

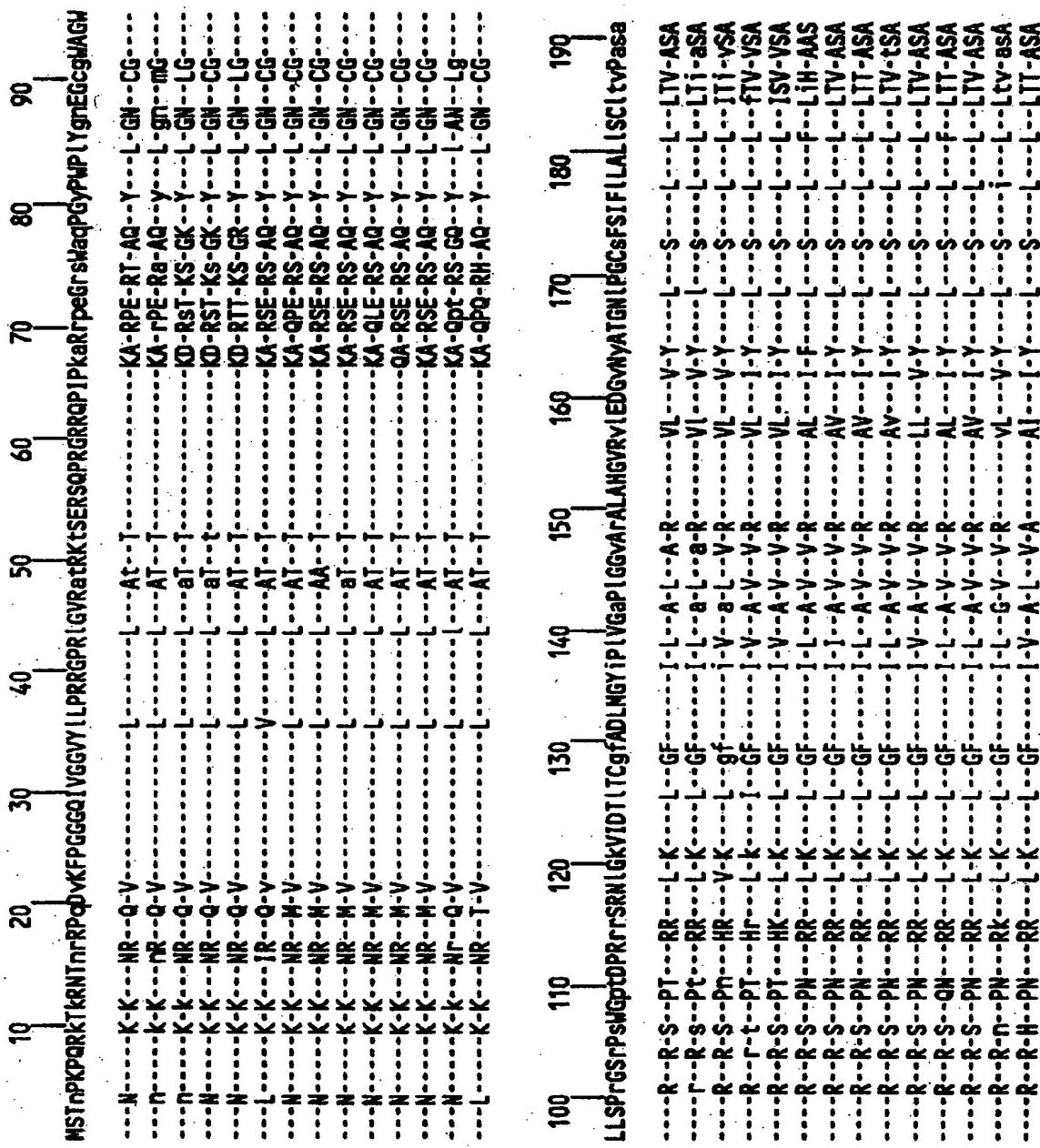


FIGURE 7K

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1...

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<u>SEQ</u>	<u>ID NO:</u>	<u>Genotype</u>
155-160	I/1a	I/1b
161-176	II/1b	III/2a
177-180	IV/2b	
181-185	2c	(V)/3a
186	190	
187	191	4a
188	192	4b
189	193	4c
190	194	4d
191	195	4e
192	196	4f
193	197	5a
194	198-205	
195	206	



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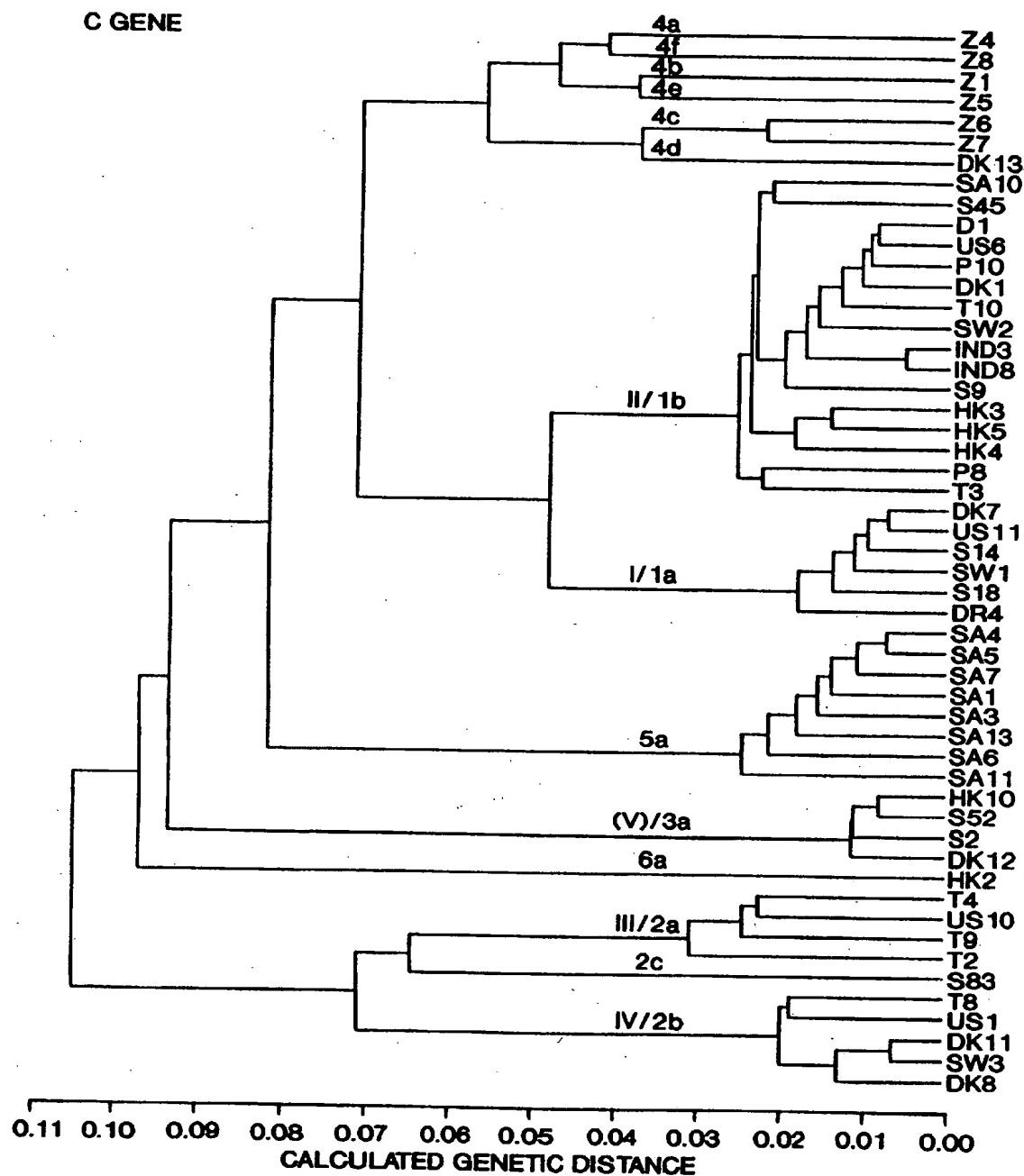
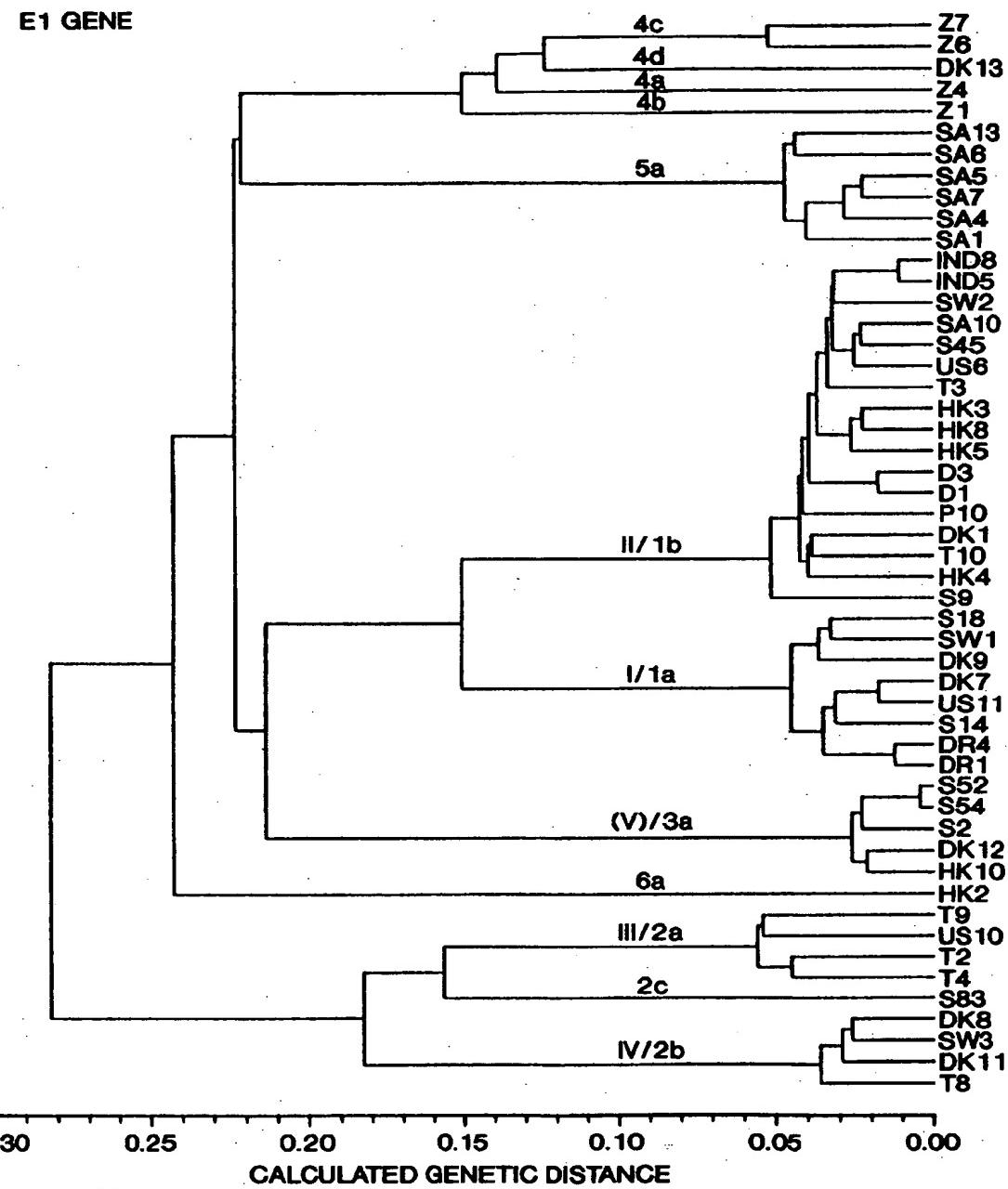


FIG. 8A

**FIG. 8B**



**NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 1A-1

<u>SEQ ID NO.:</u>	<u>Isolate</u>	<u>S14</u>
5		
1	DK7	
8	US11	
4	DR4	
3	DR1	
2	DK9	
6	S18	
7	SW1	
1-8	consensus	
<u>SEQ ID NO.:</u>	<u>Isolate</u>	<u>S14</u>
5		
1	DK7	
8	US11	
4	DR4	
3	DR1	
2	DK9	
6	S18	
7	SW1	
1-8	consensus	

1 TACCAAGTGGCAACTCCAGGGGCTTTACCATGTTACCAATGATTGCCCTAACTCGAGTA
1 TACCAAGTGGCAACTCCAGGGGCTTTACCATGTTACCAATGATTGCCCTAACTCGAGTA
1 TACCAAGTGGCAACTCCAGGGGCTTTACCATGTTACCAATGATTGCCCTAACTCGAGTA
1 TACCAAGTGGCAACTCCAGGGGCTCTACGGGCTTACCATGTTACCAATGATTGCCCTAACTCGAGTA
1 CACCAAGTGGCAACTCTAACGGGCTCTACGGGCTTACCATGTTACCAATGATTGCCCTAACTCGAGTA
1 TACCAAGTGGCAACTCCTGGGGCTCTACCGGCTTACCATGTTACCAATGATTGCCCTAACTCGAGTA
1 TACCAAGTGGCAACTCCAGGGCTTACCATGTTACCAATGACTGCCCTAACTCGAGCA
1 TACCAAGTGGCAACTCCAGGGCTTACCATGTTACCAATGATTGCCCTAACTCGAGTA

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FIGURE 1A-2

<u>SEQ ID NO:</u>	<u>Isolate</u>		
5	S14		
1	DK7	123	GGGTAACacCTCGAACTGGTGGCCATGACCCCCACGGTGGCCACCAAGGGACGGCAA
8	US11	123	GGGTAACGtCTCGAGGTGGTGGCGATGACCCCACGGTGGCCATGACCCCCACGGGAA
4	DR4	123	GGGTAACGctTCGAGGTGGTGGCGATGACCCCACGGTGGCCACCAAGGGACGGCAA
3	DR1	123	GGGTAACGCTCGAGGTGGTGGCGATGACCCCACGGTGGCCACCAAGGGACGGCAA
2	DK9	123	GGGTAACGCTCGAGGTGGTGGCGATGACCCCACGGTGGCCACCAAGGGACGGCAA
6	S18	123	GGGTAACGCTCGAGATGGTGGGTGGCGTGGGTGGCGTGGGTGGCGTGGGTGGCGTGG
7	SW1	23	GGAATggGCCCGAAatGTTGGTGGTGGGTGGCGTGGGTGGCGTGGGTGGCGTGG
1-8	consensus		GGgttaaCgcctCGAaggTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
<u>SEQ ID NO:</u>	<u>Isolate</u>		
5	S14	184	CTCCCCGCAacCGCACCTCGACGTtACATGATCTGGATCTGGTtGTGGAGGCCACCCCTCTGTT
1	DK7	184	CTCCCCCAAGCGCACCTCGACGTtACATGATCTGGTtGTGGAGGCCACCCCTCTGTT
8	US11	184	CTCCCCCAAGCAACTTCAAGCTtACATGATCTGGTtGTGGAGGCCACCCCTCTGTT
4	DR4	184	CTCCCCCAAAAGCAAGCAGCTtCGACGTtACATGATCTGGTtGTGGAGGCCACCCCTCTGTT
3	DR1	184	CTCCCCCAAAAGCAAGCAGCTtCGACGTtACATGATCTGGTtGTGGAGGCCACCCCTCTGTT
2	DK9	184	CTCCCCGAAAGCAAGCTtCGACGTtACATGATCTGGTtGTGGAGGCCACCCCTCTGTT
6	S18	184	CTCCCCGAAAGCAAGCTtCGACGTtACATGATCTGGTtGTGGAGGCCACCCCTCTGTT
7	SW1	184	CTCCCTGAAACGCAGTTCAACGTtACATGATCTGGTtGTGGAGGCCACCCCTCTGTT
1-8	consensus		CTCCCC - CAA CGCAGCTtCGACGTtACATGATCTGGTtGTGGAGGCCACCCCTCTGTT

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FIGURE 1A-3

<u>SEQ_ID NO:</u>	<u>Isolate</u>	
5	S14	245 CGGGCCCTCTACGTTGGGGACTTGTGGGGTCTGCTTTCAGCTGCGGTCAGCTGTTAACCTT
1	DK7	245 CGGGCCCTCTACGTTGGGGACCTGTGGGGTCTGCTTTCAGCTGCGGTCAGCTGTTAACCTT
8	S11	245 CGGGCCCTCTACGTTGGGGACCTGTGGGGTCTGCTTTCAGCTGCGGTCAGCTGTTAACCTT
4	DR4	245 CGGGCCCTCTACGTTGGGGACTTGTGGGGTCTGCTTTCAGCTGCGGTCAGCTGTTAACCTT
3	DR1	245 CGGGCCCTCTACGTTGGGGACCTGTGGGGTCTGCTTTCAGCTGCGGTCAGCTGTTAACCTT
2	DK9	245 CGGGCCCTCTACGTTGGGGACTTGTGGGGTCTGCTTTCAGCTGCGGTCAGCTGTTAACCTT
6	S18	245 CGGGCCCTCTACGTTGGGGACCTGTGGGGTCTGCTTTCAGCTGCGGTCAGCTGTTAACCTT
7	SW1	245 CGGGCCCTCTACGTTGGGGACCTGTGGGGTCTGCTTTCAGCTGCGGTCAGCTGTTAACCTT
1-8	consensus	CGGGCCCTCTACGTTGGGGACCTGTGGGGTCTGCTTTCAGCTGCGGTCAGCTGTTAACCTT
<u>SEQ_ID NO:</u>	<u>Isolate</u>	
5	S14	306 CTCTCCAGGGGCCCTGTGCAAGACTGCAATTGTCTATCTATCCGGCCATATA
1	DK7	306 CTCCTCCAGGGCCACTGGCAAGGCTGCAATTGTCTATCTATCCGGCCATATA
8	S11	306 CTCCTCCAGGCAAGCCACTGGCAAGGCTGCAATTGTCTATCTATCCGGCCATATA
4	DR4	306 CTCCTCCAGGCAAGCCACTGGCAAGGCTGCAATTGTCTATCTATCCGGCCATATA
3	DR1	306 TCTCTCCAGGGCCACTGGCAAGGCTGCAATTGTCTATCTATCCGGCCATATA
2	DK9	306 CTCCTCCAGGGCAACTGGCAAGGACTGCAACTGGCAATTGTCTATCTATCCGGCCATATA
6	S18	306 CTCCTCCAGGGCCACTGGCAAGGACTGCAATTGTCTATCTATCCGGCCATATA
7	SW1	306 CTCCTCCAGGGCCACTGGCAAGGACTGCAATTGTCTATCTATCCGGCCATATA
1-8	consensus	CTCTCCAGGGCCACTGGCAAGACTGCAATTGTCTATCTATCCGGCCATATA

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FIGURE 1A-4

<u>SEQ_ID NO:</u>	<u>Isolate</u>	<u>SEQ_ID NO:</u>	<u>Isolate</u>
5	S14	367	ACGGGTCAATGCCATGGCATGGATATGATGAACTGGTCCCCCTACgACGGGactGGTAG
1	DK7	367	ACGGGTCACCGCATGGCATTGGcgTGGCATATGATGAACTGGTCCCCCTACcACGGGCTGGTAG
8	S11	367	ACGGGTCACCGCATGGCATTGGCATGGCATTGGCATATGATGAACTGGTCCCCCTACGGGCTGGTAG
4	DR4	367	ACGGGCACCGCATGGCATGGGATTGGCATATGATGAACTGGTCCCCCTACGACAGGGCTGGTAG
3	DR1	367	ACGGGaACCGtATGGCATGGGATTGGCATATGATGAACTGGTCCCCCTACGACAGGGCTGGTA
2	DK9	367	ACGGGTCAATGCCATGGGATTGGCATATGATGAACTGGTCCCCCTACAGCAGGGCTGGTAG
6	S18	367	ACGGGTACCGtATGGCATGGGATTGGCATATGATGAACTGGTCCCCCTACAAACGGGtTGTTAA
7	SW1	367	ACGGGTACCGCATGGGATTGGCATATGATGAACTGGTCCCCACAACAGGGctCTGGTAG
1-8	consensus		ACGGGtCACCGCATGGCATGGGATTGGCATGGGACTGGTCCCCtACgAC-GGcgCTGGTAG
5	S14	428	TAGCTCAGCTCGGATCCCACAGCCATCTTGGATATGATCGCTGGTGTACTGGGG
1	DK7	428	TAGCTCAGCTCGGATCCC9CAAGCCATCTTGGACATGATCGCTGGTGTACTGGGG
8	S11	428	TAGCTCAGCTCGGATCCCACAGCCATCTTGGACATGATCGCTGGTGTACTGGGG
4	DR4	428	TAGCTCAGCTCGGATCCCACAGCCATCTTGGACATGATCGCTGGTGTACTGGGG
3	DR1	428	TGGCTCAGCTCGGATCCCACAGCCATCTTGGACATGATCGCTGGTGTACTGGGG
2	DK9	428	TGGGcgAGGCTCGTcAGGATCCCAGCCATCTTGGACATGATCGCTGGTGTACTGGGG
6	S18	428	TAGCTCAGCTCGTcAGGtTCCCAGCCAGGGTGGACATGATCGCTGGTGTACTGGGG
7	SW1	428	TAGCTCAGCTCGTcAGGtTCCCAGGGTGGACATGATCGCTGGTGTACTGGGG
1-8	consensus		TagGtCAGCTGCTCCGGatTCCC-CAAGCCAtCTTGGACATGATCGCTGGtGCCACTGGGG

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FIGURE 1A-5

<u>SEQ ID NO:</u>	<u>Isolate</u>		<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	489 AGTCCTaGGGGCATAGCGTATTTCCTCCATGGTGGGAAACCTGGGGAAAGGTCTaGTggTG	5	S14	550 CTCGCTGGCTATTTCGCCGGGTTGACGGCG
1	DK7	489 AGTCCTGGGGCATAGCGTATTTCCTCCATGGTGGGAAACTGGGGAAAGGTCTGGTAGTG	1	DK7	550 CTGCGCTGGCTATTTCGCCGGGTTGACGGCG
8	S11	489 AGTCCTAGGGGCATAGCGTATTTCCTCCATGGTGGGAAACTGGGGAAAGGTCTGGTAGTG	8	US11	550 CTGCGCTGGCTATTTCGCCGGGTTGACGGCG
4	DR4	489 AGTCCTAGGGGCATAGCGTATTTCCTCCATGGTGGGAAACTGGGGAAAGGTCTGGTAGTG	4	DR4	550 CTGCGCTGGCTATTTCGCCGGGTTGACGGCG
3	DR1	489 AGTCCTAGGGGCATAGCGTATTTCCTCCATGGTGGGAAACTGGGGAAAGGTCTGGTAGTG	3	DR1	550 CTGCGCTGGCTATTTCGCCGGGTTGACGGCG
2	DK9	489 AGTCCTAGGGGCATAGCGTATTTCCTCCATGGTGGGAAACTGGGGAAAGGTCTGGTAGTG	2	DK9	550 CTGCGCTGGCTATTTCGCCGGGTTGACGGCG
6	S18	489 AGTCCTAGGGGCATAGCGTATTTCCTCCATGGTGGGAAACTGGGGAAAGGTCTGGTAGTG	6	S18	550 CTGCGCTGGCTATTTCGCCGGGTTGACGGCG
7	SW1	489 AGTCCTAGGGGCATAGCGTATTTCCTCCATGGTGGGAAACTGGGGAAAGGTCTGGTAGTG	7	SW1	550 CTGCGCTGGCTATTTCGCCGGGTTGACGGCG
1-8	consensus	AGTCCTaGGGGCATAGCGTATTTCCTCCATGGTGGGAAACTGGGGAAAGGTCTGGTAGTG	1-8	consensus	CTGTTGCTGGTttgCCGGGTTGATGCG

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FIGURE 1B-1

<u>SEQ_ID NO.:</u>	<u>Isolate</u>	
11	DK1	
24	T10	1 TATGAAGTGGCAAACGTTCCGGGTGTACCACTGTCACAAACGACTGCTCCAACTCAAGCA
10	D3	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGCA
9	D1	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCGAGCA
14	HK5	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTtAAGCA
15	HK8	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGCA
12	HK3	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGCG
23	T3	1 TACGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGCA
22	SW2	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGCA
17	IND8	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGTA
16	IND5	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGTA
21	SA10	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGCA
20	S45	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGCA
25	US6	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGCA
13	HK4	1 CATGAAGTGCACAACTGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGTA
18	P10	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGTA
19	S9	1 TATGAAGTGGCAAACGTTCCGGGTGTACCAATGTACCGAACGACTGCTCCAACTCAAGTA
9-25	consensus	tATGAAGTGGCAAACGTTCCGGGTgtTACCATGTCAACGAAACGACTGCTCCAACTcaAGca

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FIGURE 1B-2

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	62 TcGTGTatGAGGGCAGtGGACtGTGATCATGCAtACCCaGGGtGGGTGCCTGCGTtCGGGA
24	T10	62 TtGTGTttTGAGGtAGGGGACTGTATGCAtGCAcACCCCtGGGTGGTtGCGTtCGGGA
10	D3	62 TcGTGTatGAGACAGGGGACATGTATGCAcACCCtGGGTGGTtGCGTtCGGGA
9	D1	62 TtGTGTatGAGACAGGGGACATGTATGCAcACCCtGGGTGGTtGCGTtCGGGA
14	HK5	62 TCGtGTACtGAGACAaGGGACATGTATGCAcACCCtGGGTGGTtGCGTtCGGGA
15	HK8	62 TCGtGTatGAAaACAGGGGACATGTATTATGCAtACCCtGGATGGcargCCtGCGTtCGGGA
12	HK3	62 TCGtGTatGAGACAGGGAGACATGTATGCAtACCCtGGATGGTtGCGTtGCGTtCGGGA
23	T3	62 TTGTGTatGAGACAGGGGACATGTATGCAcACCCtGGGTGGTtGCGTtGCGTtCGGGA
22	SW2	62 TTGTGTatGAGACAGGGGACATGTATGCAcACCCtGGGTGGTtGCGTtGCGTtCGGGA
17	IND8	62 TTGTGTatGAGGCAAGGGGACATGTATGCAcACCCtGGGTGGTtGCGTtGCGTtCGGGA
16	IND5	62 TTGTGTatGAGGCAAGGGGACATGTATGCAcACTCCGGGTGGTtGCGTtGCGTtCGGGA
21	SA10	62 TTGTGTatGAGGCAAGGGGACATGTATGCAcACTCCGGGTGGTtGCGTtGCGTtCGGGA
20	S45	62 TTGTGTatGAGGCAAGGGGACtGTGATCATGCAcACCCtGGGTGGTtGCGTtGCGGGA
25	US6	62 TTGTGTatGAGGCAAGGGGACATGTATGCAcACTCCGGGTGGTtGCGTtGCGTtCGGGA
13	HK4	62 TTGTGTatGAGGCAAGGGGACATGTATGCAcACTCCGGGTGGTtGCGTtGCGTtCGGGA
18	P10	62 TTGTGTatGAGGCAAGGGGACATGTATGCAcACTCCGGGTGGTtGCGTtGCGTtGTTCaGGA
19	S9	62 TTGTGTatGAGGCAAGGGGACtGTATGCAcACCCCCGGGTGcg9TgCCCTGCGTtCGGGA
9-25	consensus	

FIGURE 1B-3

SEQ_ID NO:	Isolate		
11	DK1	123	GaaCAACcaCTCCCGTGTCTGGGTAGGGCTCACccCACGCTCGGGCAGGCCAGC
24	T10	123	GGGAAACTCTCCCGCTGCTGGTAGGGCTCACccCACGCTCGGGCAGGCCAGC
10	D3	123	GGACAACCTCCCTCTCGCTGTGGTAGGGCTCACccCACGCTCGGGCTAGGAATGGCAGC
9	D1	123	GGACAACCTCCCTCTCGCTGTGGTAGGGCTCACccCACGCTCGGGCTAGGAATGGCAGC
14	HK5	123	AAACAACCTCCCGTTGTGGTAGGGCTGGCTCACTCCACGCTCGGGCTAGGAATGGCAGC
15	HK8	123	GAACAACCTCCCGTTGTGGTAGGGCTGGCTCACTCCACGCTCGGGCTAGGAATGGCAGC
12	HK3	123	GAACAACCTCCCGCTGTGGTAGGGCTCACTCCACGCTCGGGCAGGAACGGTCAGC
23	T3	123	GAGCAATTCCCTCCCGCTGTGGTAGGGCTACTCCACGCTCGGGCTAGGAACGCCAGC
22	SW2	123	GGCCAACCTCCCGCTGTGGTAGGGCTCACTCCACGCTCGGGCTAGGAACGCCAGC
17	IND8	123	GGGCAACCTCCCTCTAGTGTGGTAGGGCTCACTCCACGCTCGGGCTAGGAACGCCAGC
16	IND5	123	GGGCAACCTCCCTCTAGTGTGGTAGGGCTCACTCCACGCTCGGGCTAGGAACGCCAGC
21	SA10	123	GAACAACCTCCCGCTGTGGTAGGGCTCACTCCACGCTCGGGCTAGGAACGCCAGC
20	S45	123	GAACAACCTCCCTCTAGTGTGGTAGGGCTCACTCCACGCTCGGGCTAGGAACGCCAGC
25	US6	123	GAACAATTCCCTCCCGCTGTGGTAGGGCTCACTCCACGCTCGGGCTAGGAACGCCAGC
13	HK4	123	GAACAACCTCCCTCCCGCTGTGGTAGGGCTCACTCCACGCTCGGGCTAGGAATCCGC
18	P10	123	GAACAACCTCCCTCCCGCTGTGGTAGGGCTCACTCCACGCTCGGGCTAGGAATCCGC
19	S9	123	GgtAACTCCTCCaaATGCTGGTggGGTAGGGCTCACCCACGCTCGGGCAGGAACgCTacc
9-25	consensus		gaacaAAactcCTCcgcTGCTGGTAGGGCTactccAACGCTCGGGCAGGAACGCCAGC

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FIGURE 1B-4

SEQ ID NO:	Isolate	ID NO:
11	DK1	184
24	T10	184
10	D3	184
9	D1	184
14	HKS	184
15	HK8	184
12	HK3	184
23	T3	184
22	SW2	184
17	IND8	184
16	IND5	184
21	SA10	184
20	S45	184
25	US6	184
13	HK4	184
18	P10	184
19	S9	184
		consensus

**NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 1B-5

SEQ ID NO:	Isolate	Length	Sequence
11	DK1	245	CCGCTATGTACGTGGGGACCTCTGGGATCCTCGTCTCACCTT
24	T10	245	CCGCTATGTatGAGGAAACCTCTGGGATCCTCGTCTCACCTT
10	D3	245	CCGCCATGTACGTGGGGATCTTGGAATCTCCAGCTGTCACTT
9	D1	245	CCGCCATGTACGTGGGGATCTTGGAATCTCCAGCTGTCACTT
14	HK5	245	CCGCTATGTACGTGGGGATCTTGGAATCTCCAGCTGTCACTT
15	HK8	245	CCGCTATGTACGTGGGGATCTTGGAATCTCCAGCTGTCACTT
12	HK3	245	CCGCTATGTACGTGGGGATCTTGGAATCTCCAGCTGTCACTT
23	T3	245	CCGCTATGTACGTGGGGATCTTGGAATCTCCAGCTGTCACTT
22	SW2	245	CCGtATGTACGTGGGGATCTTGGAATCTCCAGCTGTCACTT
17	IND8	245	CCGCTATGTACGTGGGGATCTTGGAATCTCCAGCTGTCACTT
16	IND5	245	CCGCTATGTACGTGGGGATCTTGGAATCTCCAGCTGTCACTT
21	SA10	245	CCGCCATGTACGTGGGGACCTCTGGGATCCTCGTCTCACCTT
20	S45	245	CCGCTATGTACGTGGGGATCTCTGGGATCCTCGTCTCACCTT
25	US6	245	CCGCTATGTACGTGGGACCTCTGGGATCCTCGTCTCACCTT
13	HK4	245	CCGcCATGTACGTGGGAGATCTGGGATCCTCGTCTCACCTT
18	P10	245	CCGCTATGTACGTGGGAGATCTGGGATCCTCGTCTCACCTT
19	S9	245	CCGCTATGTACGTGGGAGATCTGGGATCCTCGTCTCACCTT
	consensus		CCGCTATGTACGTGGGGAGATCTGGGATCCTCGTCTCACCTT

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF

THE ENVELOPE 1...

Bukh et al.

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FIGURE 1B-6

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 1B-7

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
11	DK1	TCAAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAACAGGCCCTAGTGC
24	T10	367 TCAGGTCAACGGCATGGCTTGGGACATGATGAACTTGCACCTACAACAGCTCTAGTGG
10	D3	367 ACAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAACAGCCCTAGTGG
9	D1	367 ACAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAACAGCCCTAGTGG
14	HK5	367 ACAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAACAGCCCTAGTGG
15	HK8	367 TCAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAACAGCCCTAGTGG
12	HK3	367 TCAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAAGCAGGCCCTAGTGG
23	T3	367 acAGGTCAACGGtATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAacCGCaCTAGTGG
22	SW2	367 TCAGGTCAACGGCATGGCTTGGGACATGATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG
17	IND8	367 TCAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG
16	IND5	367 TCAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG
21	SA10	367 ACAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG
20	S45	367 ACAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG
25	US6	367 TCAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG
13	HK4	367 TCAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG
18	P10	367 TCAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG
19	S9	367 acAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG
9-25	consensus	tCAAGGTCAACGGCATGGCTTGGGATATGATGAACTTGATGAACTTGCACCTACAGCAGGCCCTAGTGG

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THE ENVELOPE 1...

Bukh et al.

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FIGURE 1B-8

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
11	DK1	
24	T10	428 TATCGCAGTTACTCCGAACTGGTGTGGACATGGTg-CGGGCCCACTGGGG
10	D3	428 T9TCGCAGTTACTCCGGATCCACAAGCTGTCAATGGACATGGTgCaGGGGCCCACGTGGGG
9	D1	428 TATCGCAGTTACTCCGGATCCACAAGCTGTGGACATGGTGGGGCCCACTGGGG
14	HK5	428 TATCGCAGTTACTCCGGATCCACAAGCTGTGGACATGGTgCaGGGGCCCACGTGGGG
15	HK8	428 TGTTCGCAGTTACTCCGGATCCACAAGCTGTGGACATGGTGGGGCCCACTGGGG
12	HK3	428 TGTTCGCAGAACTACTCCGGATCCACAAGCTGTGGACATGGTgCaGGGGCCCACGTGGGG
23	T3	428 TGTTCGCAGTTACTCCGGATCCACAAGCTGTGGACATGGTGGGGCCCACTGGGG
22	SW2	428 TATCGCAGTTACTCCGGATCCACAAGCTGTGGACATGGTgCaGGGGCCCACGTGGGG
17	IND8	428 TATCGCAGTTACTCCGGATCCACAAGCTGTGGGGATATGGTGGGGCCCACTGGGG
16	IND5	428 TATCGCAGTTACTCCGGATCCACAAGCTGTGGGGATATGGTGGGGCCCACTGGGG
21	SA10	428 TATCGCAGTTACTCCGGATCCACAAGCTGTGGACATGGTGGGGCCCACTGGGG
20	S45	428 TATCGCAGTTACTCCGGATCCACAAGCTGTGGACATGGTGGGGCCCACTGGGG
25	US6	428 TATCGCAGTTACTCCGGATCCACAAGCTGTGGGGCCCACTGGGG
13	HK4	428 TATCGCAGTTACTCCGactTCGGATCTGGACATGGTGTCAATGGGAGCCCACTGGGG
18	P10	428 T9TCGCAGGTACTCCGGATCCACAAGCTGTGGATCTGGATGTGGTGGGGCCCACTGGGG
19	S9	428 TATCGCAGGTACTCCGGATCCACAAGCTGTGGATATGGTGGGGCCCACTGGGG
9-25	consensus	TatTCGCAGgtTactCCGGatCCACAAGCTgtCTGGAcataGGTgCggggGCCCCACTGGGG

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FIGURE 1B-9

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	
24	T10	489 AGTCCTGGGGCCCTGCCTACTACTCCATGGGGAACTGGGCCAAGGTTTAATTGTG
10	D3	489 AGTCCTGGGGCCCTGCCTACTATTCCATGGGGAACTGGCTAACGGTTAACGGTGTG
9	D1	489 GGTCTGGGGCCCTGCCTACTATTCCATGGGGAACTGGCTAACGGTTAACGGTGTG
14	HK5	489 GGTCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
15	HK8	489 AGTCCTAGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
12	HK3	489 AGTCCTAGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
23	T3	489 AGTCCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
22	SW2	489 AGTCCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
17	IND8	489 AATCCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
16	IND5	489 AATCCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
21	SA10	489 AGTCCTAGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
20	S45	489 AGTCCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
25	US6	489 AGTCCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
13	HK4	489 AGTCCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
18	P10	489 AGTCCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
19	S9	489 AGTCCTGGGGCCCTGCCTACTATTCCATGGGGAAACTGGCTAACGGTTAACGGTGTG
9-25	consensus	agtccctggggccctgcctactattccatggggaaactggctaacggtaaggtttgattgtg

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FIGURE 1B-10

<u>SEQ_ID NO.:</u>	<u>Isolate</u>	
11	DK1	550 tTGCTACTCTTGCAGGGTTGATGGG
24	T10	550 ATGCTACTCTTGCAGGGTTGATGGG
10	D3	550 ATGCTACTCTTGCAGGGTTGATGGG
9	D1	550 ATGCTACTCTTGCAGGGTTGACGGC
14	HK5	550 ATGCTACTCTTGCAGGGTTGATGGG
15	HK8	550 ATGCTACTCTTGCAGGGTTGATGGG
12	HK3	550 ATGCTACTCTTGCAGGGTTGATGGG
23	T3	550 CTGCTACTCTTGCAGGGTTGATGGG
22	SW2	550 ATGCTACTCTTGCAGGGTTGACGGG
17	IND8	550 ATGCTACTCTTGCAGGGTTGACGGG
16	IND5	550 ATGCTACTCTTGCAGGGTTGACGGG
21	SA10	550 ATGCTACTCTTGCAGGGTTGACGGG
20	S45	550 ATGCTACTCTTGCAGGGTTGACGGG
25	US6	550 tTGCTACTCTTGCAGGGTTGACGGG
13	HK4	550 ATGCTACTCTTGCAGGGTTGACGGG
18	P10	550 ATGCTACTCTTGCAGGGTTGACGGGa
19	S9	550 ATGCTACTCTTGCAGGGTTGACGGG
	consensus	atGCTACTCTTGCAGGGTTGACGGG

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FIGURE 1C-1

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 1C-2

<u>SEQ_ID NO:</u>	<u>Isolate</u>		
26	T2	184	GCTCTtACGGAGGGCTTGCAGGCAATcGACATGGATGTCGGCACGCCACGGCTCTGCT
27	T4	184	GCCCTCAAGCGAGGGCTTGCAGGCAATtGACATGGATGTTGTGATGTCGGCACGCCACGGCTCTGCT
28	T9	184	GCCCTCAAGCGAGGGCTTGCAGGCAATcGACATGGATGTCGGCACGCCACGGCTCTGCT
29	US10	184	GCCCTCAAGCGAGGGCTTGCAGGCAACTCACATGACATGGATGTCGGATGTCGGCACGCCACGGCTCTGCT
26-29	consensus		GCCCTCAAGCGAGGGCTTGCAGGACACATGACATGGATGTCGGATGTCGGCACGCCACGGCTCTGCT
<u>SEQ_ID NO:</u>	<u>Isolate</u>		
26	T2	245	CTGCCCTtTACGTGGGGACCTCTGGGGGTGATGCTGGAGCCAGATGTTCATtGT
27	T4	245	CTGCTCTtTACGTGGGGACCTCTGGGGTGATGCTGGAGCCAGATGTTCATCGT
28	T9	245	CCGCTCTtTACGTGGGGATCTCTGGGGTaATGCTGGCCGCTCAGATGTTCATTA
29	US10	245	CCGCTCTtTACGTGGGGACTCTGGGGTGGATGCTGGCTGGAGCCAAATGTTCATTT
26-29	consensus		C-GCTCT-TACGTGGGGACCTCTGGGGTGATGCTGGAGCCAAATGTTCATTT
<u>SEQ_ID NO:</u>	<u>Isolate</u>		
26	T2	306	CTGCCGGGAGCCACTGGTTGTGCAAGAATTGCAATTGCTCCATCTACCCGGTACCATC
27	T4	306	CTGCCGGAACATCACTGGTTGTGCAAGACTGCAATTGCTCATCTACCCGGTACCATC
28	T9	306	CTGCCGGAGCACCACCTGGTTGTGCAAGGAATTGCAACTGCTCCATTACCCGGTACCATC
29	US10	306	CTGCCGGGCCACCAACTGTTGTGCAAGGAATTGCAACTGCTCCATTACCCGGTACCATC
26-29	consensus		CTGCCGGC-aAccCAGTGGTTGTGCA-GAatGCAA-TGCTCCATCTACCC-GGTACCATC

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FIGURE 1C-3

<u>SEQ ID NO.:</u>	<u>Isolate</u>			
26	T2	367	ACTGGACACCGTATGGGACATGGTATGATGAACTGGTCGCCACAGCCACCATGATCC	
27	T4	367	ACTGGACACCGTATGGCATGGGATATGATGAACTGGTCGCCACAGCCACCATGATCC	
28	T9	367	ACTGGACACCGTATGGCATGGGACATGGTATGATGAACTGGTCGCCACAGCCACCATGATCT	
29	US10	367	ACCGGGCACCGTATGGCATGGGACATGGTATGATGAACTGGTCGCCACAGGGCACCTTGATCC	
26-29	consensus		ACtGGACACCGTATGGGACATGGTATGATGAACTGGTCGCCAC-gCCACCATGATCC	
<u>SEQ ID NO.:</u>	<u>Isolate</u>			
26	T2	428	TGGCGTAGCGGATGCGGTTCCCGAGGTATCATAGACATCATCGGCGGGCTCACTGGGG	
27	T4	428	TGGCGTAGCGGATGCGGTTCCCGAGGTATCATGACATCGTTAGCGGGGCaCACTGGGG	
28	T9	428	TGGCGTAGCGGATGCGGTTCCCGAGGTATCATAGACATCATCGGGGGCTCACTGGGG	
29	US10	428	TGGCGTAGCGGATGCGGTTCCCGAGGTATCATAGACATCATCGGGGGCTCACTGGGG	
26-29	consensus		TGGCGTAGCGGATGCGGTTCCCGAGGTATCATAGACATCATCGGGGGCTCACTGGGG	
<u>SEQ ID NO.:</u>	<u>Isolate</u>			
26	T2	489	CGTCATGTTGGCTTGCCTACTTCTCTATGCAGGGAGCGTGGGGAAAGGTCAATTGTCATC	
27	T4	489	CGTCATGTTGGCTTGCCTACTTCTCTATGCAGGGAGCGTGGGGAAAGGTCAATTGTCATC	
28	T9	489	CGTCATGTTGGCTTGCCTACTTCTCTATGCAGGGAGCGTGGGGAAAGGTCAATTGTCATC	
29	US10	489	CGTCATGTTGGCTTGCCTACTTCTCTATGCAGGGAGCGTGGGGAAAGGTCAATTGTCATC	
26-29	consensus		CGTCATGTTGGCTT-GCCTACTTCTCTATGCAGGGAGCGTGGGGAA-GTCGTTGTCATC	

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FIGURE 1C4

<u>SEQ ID NO:</u>	<u>Isolate</u>	
26	T2	550 CTctTGCTGGCTGCTGGGGTGGACCGCG
27	T4	550 CTTCTGGCCGGCTGGGGTGGACCGCG
28	T9	550 CTgtTGCTaccGGCTGGGGTGGACCGCG
29	US10	550 CTTCTGGCTagCCGGCTGGGGTGGACCGCG
26-29	consensus	CTT-TGCTggCCGGCTGGggGTGGACCGCG

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FIGURE 1D-1

<u>SEQ ID NO:</u>	<u>Isolate</u>		
33	T8		
30	DK8	1	GTTGGAAAGTtAGaAACACCCAGTTtAGCTTACTACGCCACCAATGATTGGCTCGAACAAACAGCA
32	SW3	1	GTGGGAAGTCAGGAACATCAGTTCCAGTACTAGCTTAGCTACTATGCCACCAATGATTGGCTCAAACAGCAGCA
31	DK11	1	GTGGGAAGTCAGGAACACCAGTTCTAGTTACTACGCCACCAATGATTGGCTCAAACAAACAGCA
30-33	consensus		GTGGGAAGTCAGGAACA-CAGTTctAGctACTACGCCACCAATGATTGGCTCAAACAAACAGCA
<u>SEQ ID NO:</u>	<u>Isolate</u>		
33	T8	62	TCACCTGGCAgCTCACCAACGCCAGTTCTCCACCTTCGGATGCGTCCCATGTGAGAATGA
30	DK8	62	TCACCTGGCAACTCACCGAACCGAGTTCTCCACCTTCGGATGCGTCCCATGTGAGAATGA
32	SW3	62	TCACCTGGCAACTCACCAACGCCAGTcCTCCACCTTCGGATGCGTCCCGTGTGAGAATGA
31	DK11	62	TCACCTGGCAACTCACCAACGCCAGTTCTCCACCTTCGGATGCGTCCCATGTGAGAATGA
30-33	consensus		TCACCTGGCAactCACCAACGCCAGTTCTCCACCTTCGGATGCGTCCCATGTGAGAATGA
<u>SEQ ID NO:</u>	<u>Isolate</u>		
33	T8	123	CAATGGCACCTTGCGGCTGCTGGATAACAAGTtaACACCTAACGGTAAACACCGTGGC
30	DK8	123	CAATGGCACCCCTGGCTGCTGGATAACAAGTGAACCTAACGGTAAACACCGGGC
32	SW3	123	tAAATGGCACCCCTGCAACTGCTGGATAACAAGTGAACCTAACGGTAAACACCGGGC
31	DK11	123	CAATGGCACCCCTGCAACTGCTGGATAACAAGTGAACCTAACGGTAAACACCGGGC
30-33	consensus		CAATGGCACCCCTGC-CTGCTGGATAACAAGTgACACCTAACGGTAAACACCGGGC

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FIGURE 1D-2

<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	184 GCACCTCACTCACAACTGGAAACgCATGTGAGCAGTATCGTAATGGCAGCTACGGTCTGCT
30	DK8	184 GCACCTACTCATAACCTGGAAACACACGTCGAGCTACGGTCTGCT
32	SW3	184 GCGCTCACTCACAACTGGAGACACGTCGATAATCGTAATGGCAGCTACGGTCTGCT
31	DK11	184 GCACCTCACTCACAACTGGAGACACGTCGATAATCGTAATGGCAGCTACGGTCTGCT
30-33	consensus	GGaCTcACTCACAACTGGGA-CaCA-gtCGA--TGATcGTAATGGCAGCTACGGTCTGCT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	245 CGGCCTTGTATGTGGGGGACGTTGCGGGCCGTTGATGATAAGGTCGAGGCTtTCATAAT
30	DK8	245 CGGCCTTGTATGTGGGAGACGTTGCGGGCCGTTGATGATCGGTGTCGAGGCTtTCATAAT
32	SW3	245 CGGCCTTGTATGTGGGAGACATGTGGGGCCGTTGATGATCGGTGTCGAGGCTtTCATAAT
31	DK11	245 CGGCCTTGTATGTGGGAGACATGTGGGGCCGTTGATGATCGGTGTCGAGGCTtTCATAAT
30-33	consensus	CGGCCTTGTATGTGGGGACGTTGCGGGCCGTTGATGATCGGTGTCGAGGCTtTCATAAT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	306 ATGCCAGAACGCCACAACCTACCCAGGAGTGCACACTGTTCCATCTACCAAGGTCAATTC
30	DK8	306 ATGCCAGAACGCCACAACCTTACCCAGGAGTGCACACTGTTCCATCTACCAAGGTCAATTC
32	SW3	306 ATGCCAGAACGCCACAACCTTACCCAGGAGTGCACACTGTTCCATCTACCAAGGTCAATTC
31	DK11	306 ATGCCAGAACGCCACAACCTTACCCAGGAGTGCACACTGTTCCATCTACCAAGGTCAATTC
30-33	consensus	ATGCCAGAACGCCACAACCTTACCCAGGAGTGCACACTGTTCCATCTACCAAGGTCAATTC

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FIGURE 1D-3

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
33	T8	
30	DK8	367 ACCGGCCACCGCATGGCATGGGACATGGATGCTgAACTGGTCAACCAACTCACCAGATCC
32	SW3	367 ACCGGCCACCGCATGGCATGGGACATGGATGCTAACTGGTCAACCAACTCACCAGATCC
31	DK11	367 ACCGGCCACCGCATGGCATGGGACATGGATGCTAACTGGTCAACCAACTCACCAGATCC
30-33	consensus	ACCGGCCACCGCATGGCATGGGACATGGATGCTAACTGGTCAACCAACTC-ACCATGATGCC

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
33	T8	428 TCGCCTAACGCtCGTGTGCTGAaCTAGtCCTtggTAaGTTGTCCTTGCGGCCATGGGG
30	DK8	428 TCGCCTATGCCGCGTGTGTTCCCTGAGCTAGGCTAGCCATTGCGGCCATGGGG
32	SW3	428 TtGCCTATGCCGCTCGTGTTCCTGAGCTAGTCTTGAAGTTGTCCTTGCGGCCATGGGG
31	DK11	428 TcGCCTATGCCGCCCGTGTTCCTGAGCTAGTCTTGAAGTGTCTGGTGGTCAATGGGG
30-33	consensus	TcGCCTATGCCGCTCGTGTCCtGAGCTAGtCCTtggTAaGTTGTCCTTGCGGCCATGGGG

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
33	T8	489 CGTGGTGTGGCTTGGCTATTCTCATGCCAAGGAGCGTGGCCAAGTCACTGCCATC
30	DK8	489 CGTGGTGTGGCTTGGCTATTCTCATGCCAAGGAGCGTGGCCAAGTCACTGCCATC
32	SW3	489 CGTGGTGTGGCTTGGCTATTCTCATGCCAAGGAGCGTGGCCAAGTCACTGCCATC
31	DK11	489 tGTGGTGTGGCTTGGCTATTCTCATGCCAAGGAGCGTGGCCAAGTCACTGCCATC
30-33	consensus	cGTGGTGTGGCTTGGCTATTCTCATGCCAAGGAGCGTGGCCA-GAGGGTGGCCA-GTCATGCCATC

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FIGURE 1D-4

<u>SEQ_ID NO.:</u>	<u>Isolate</u>	
33	T8	550 CTCCTCCTTGTGGAGGTGGACGCA
30	DK8	550 CTCCTCCTTGTGGAGGTGGATGCA
32	SW3	550 CTCCTGCTTGTGGAGGTGGATGCA
31	DK11	550 CTCCTCTTGTAGGAGGTGGATGCA
30-33	consensus	CTCCCTTCTTGTGGAGGTGGATGCA

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FIGURE 1E-1

<u>SEQ ID NO.:</u>	<u>Isolate</u>		
35	DK12	1	t TAGAGTGGGAAATGTGTCGGCCTCTACGTCCTTACCAACGACTGTt CCAATAGCAGTA
36	HK10	1	CTAGAGTGGGAAATGTGTCGGCCTCTACCAACGACTGTCCAAATAGCAGTA
37	S2	1	CTAGAGTGGGAAATACGTCTGGCCTCTATGTCTCCTACCAACGACTGTt CCAATAGCAGTA
39	S54	1	CTAGAGTGGGAAATACGTCTGGCCTCTATGTCTCCTACCAACGACTGTt CCAATAGCAGTA
38	S52	1	CTAGAGTGGGAAATACGTCTGGCCTCTATgt CTCCTACCAACGACTGTt CCAATAGCAGTA
35-39	consensus		CTAGAGTGGGAAATacGTCTGGCCTCTATgt CTCCTACCAACGACTGTt CCAATAGCAGTA
<u>SEQ ID NO.:</u>	<u>Isolate</u>		
35	DK12	62	TcGTGTATGAGGCCATGACGGCATTCCTGCACACACCTGGCTGTACTTGTGTt CAGGA
36	HK10	62	TTGTGTATGAGGCCATGACGGCATTCCTGCACACACCTGGCTGTACTTGTGTt CAGGA
37	S2	62	TTGTGTATGAGGCCATGACGGTTATTCTGGCACACCTGGCTGTACTTGTGTt CAGGA
39	S54	62	TTGTGTATGAGGCCATGACGGCATTCCTGCACACACCCGGCTGTGTACTTGTGTt CAGGA
38	S52	62	TTGTGTATGAGGCCATGACGGCATTCCTGCACACACCCGGCTGTGTACTTGTGTt CAGGA
35-39	consensus		Tt GTGTATGAGGCCATGACGGt ATTCTGGCACACACCTGGCTGTACTTGTGTt CAGGA

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FIGURE 1E-2

<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>Isolate</u>
35		DK12
36		HK10
37		S2
39		S54
38		S52
35-39		consensus

<u>SEQ_ID</u>	<u>ID NO.:</u>	<u>Isolate</u>	<u>DK12</u>
35			
36		HK10	
37		S2	
39		S54	
38		S52	
			consensus

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FIGURE 1E-3

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
35	DK12	
36	HK10	
37	S2	
39	S54	
38	S52	
35-39	consensus	
<u>SEQ ID NO.:</u>	<u>Isolate</u>	
35	DK12	
36	HK10	
37	S2	
39	S54	
38	S52	
35-39	consensus	

35	CTGGGCTCTACGTGGGTGATgtGTGCCCCGTCCTtGTGGGACAAAGCCTTACGTT	245	CTGGGCTCTACGTGGGTGATgtGTGCCCCGTCCTtGTGGGACAAAGCCTTACGTT
36	CTGGGCTCTACGTGGGCGATATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT	245	CTGGGCTCTACGTGGGCGATATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT
37	CTGGGCTCTACGTGGGTGATAATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT	245	CTGGGCTCTACGTGGGTGATAATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT
39	CTGGGCTCTATGTGGGTGATAATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT	245	CTGGGCTCTATGTGGGTGATAATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT
38	CTGGGCTCTATGTGGGTGATAATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT	245	CTGGGCTCTATGTGGGTGATAATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT
35-39	CTGGGCTCTACGTGGGTGATAATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT		CTGGGCTCTACGTGGGTGATAATGTGTGGGCCGTCCTCGTGGGACAAAGCCTTACGTT

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FIGURE 1E-4

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FIGURE 1E-5

<u>SEQ ID NO:</u>	<u>Isolate</u>	<u>SEQ ID NO:</u>	<u>Isolate</u>
35	DK12	35	DK12
36	HK10	36	HK10
37	S2	37	S2
39	S54	39	S54
38	S52	38	S52
35-39	consensus	35-39	consensus

489 CATCATGGCGGGCTAGCCTATTACTCCATGCGGGCAACTGGGCCAAGGGTCGCTATCATC
 489 CATCTTGGCaGGCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTGCTATCATC
 489 CATCTTGGGGCCTAGCCTATTACTCCATGCAaGGCAACTGGGCCAAGGTGCTATCATC
 489 CATCTTGGGGCCTAGCCTATTACTCCATGCAAGGGCAACTGGGCCAAGGTGCTATCATC
 489 CATCTTGGGGCCTAGCCTATTACTCCATGCAAGGGCAACTGGGCCAAGGTGCTATCATC

CATCTTGGGGCTAGCCTATTACTCCATGCAAGGGCAACTGGGCCAAGGTGCTATgTC

550 ATGGTTATGTTTCAGGAGTCGATGCC
 550 ATGGTTATGTTTCAGGGTGCATGCC
 550 ATGGTTATGTTTCAGGGTGCAGGCC
 550 ATGATTATGTTTCAGGGTGCATGCC
 550 ATGATTATGTTTCAGGGTGCATGCC
 550 ATGATTATGTTTCAGGGTGCATGCC

ATGGTTATGTTTCAGGGTGCATGCC

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FIGURE 1F-1

<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	1 GTcAACTATCAACATGCCCTCGGGGCTPATCACATCCAAACGACTGCCGAAACTCGAGCA 1 GTtAACTATCGCAATGCCCTCGGGCCTPATCACGTCAACAGACTGCCGAAACTCGAGCA
42	Z6	1 GTtAACTATCGCAATGCCCTCGGGCCTPATCACGTCAACAGACTGCCGAAACTCGAGCA
42-43 consensus (Z6)		GTtAACTATCGCAATGCCCTCGGGGCTPATCACGTCAACAGACTGCCGAAACTCGAGCA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	62 TaaTGTATGAGGCCAACACCATCCTACACCTCCCAGGGTGCTTACCCACCGTGGGGGcGcCTTATATCGGT 62 TAGTGTATGAGGCCAACACCATCCTACACCTCCCAGGGTGCTTACCCACCGTGGGGTGTGCTTACCCCTGTGAGGGT
42	Z6	TAGTGTATGAGGCCAACACCATCCTACACCTCCCAGGGTGCTTACCCACCGTGGGGTGTGCTTACCCCTGTGAGGGT
42-43 consensus (Z6)		TAGTGTATGAGGCCAACACCATCCTACACCTCCCAGGGTGCTTACCCACCGTGGGGTGTGCTTACCCCTGTGAGGGT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	123 gggGAACCAAGTCACGCTGCTGGGGCCCTTACTCCACCGTGGGGGcGcCTTATATCGGT 123 tGGGAATCAGTCACGCTGCTGGGGCCCTTACTCCACCGTGGGGGtGCTTATATCGGT
42	Z6	tGGGAATCAGTCACGCTGCTGGGGCCCTTACTCCACCGTGGGGGtGCTTATATCGGT
42-43 consensus (Z6)		tGGGAATCAGTCACGCTGCTGGGGCCCTTACTCCACCGTGGGGGtGCTTATATCGGT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	184 GcaccGGTTGaaATCCGGAGACATGTGGACCTTGATGGTAGGGGCTGCTAACAGTGTGCT 184 GCTCCGGTTGACTCCCTCCGGAGACATGTGGACCTTGATGGGGGCTGCTAACAGTGTGCT
42	Z6	GCTCCGGTTGACTCCCTCCGGAGACATGTGGACCTTGATGGGGGCTGCTAACAGTGTGCT
42-43 consensus (Z6)		GCTCCGGTTGACTCCCTCCGGAGACATGTGGACCTTGATGGGGGCTGCTAACAGTGTGCT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	245 CcGGtCTCTACatTTGGGACCTGTGGGGGCTGCTAACAGTGTGCT 245 CtGCCCTCTACgtTTGGAGATCTGTGGGGTGTGcATTCTTGTTGGGGAGATGCTTCTCCCTT
42	Z6	245 CtGCCCTCTACgtTTGGAGATCTGTGGGGTGTGcATTCTTGTTGGGGAGATGCTTCTCCCTT
42-43 consensus (Z6)		CtGCCCTCTACgtTTGGAGATCTGTGGGGTGTGcATTCTTGTTGGGGAGATGCTTCTCCCTT

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FIGURE 1F-2

<u>SEQ ID NO.:</u>	<u>Isolate</u>	<u>SEQ ID NO.:</u>	<u>Isolate</u>	<u>SEQ ID NO.:</u>	<u>Isolate</u>	<u>SEQ ID NO.:</u>	<u>Isolate</u>	<u>SEQ ID NO.:</u>	<u>Isolate</u>																				
43	Z7	306	CCAGCGGACGCCACTGGCACTACGGCAGGACTCGCAATTGTTCCATCTAAGCGGGCACGTT	306	CCAGCGGACGCCACTGGCACTACGGCAGGACTCGCAATTGTTCCATCTAAGCGGGCACGTT	367	AcAGGCCAACAGAAATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC	367	AcAGGCCAACAGAAATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC	367	AcGGGCCACAGGATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC																		
42	Z6	306	CCAGCGGACGCCACTGGCACTACGGCAGGACTCGCAATTGTTCCATCTAAGCGGGCACGTT	367	AcAGGCCAACAGAAATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC	428	TGCCCCAGGTATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC	428	TGCCCCAGGTATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC	428	TGCCCCAGGTATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC																		
42-43 consensus	(Z6)	CCAGCGGACGCCACTGGCACTACGGCAGGACTCGCAATTGTTCCATCTAAGCGGGCACGTT	42-43 consensus	(Z6)	AcGGGCCACAGGATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC	42-43 consensus	(Z6)	428	TGCCCCAGGTATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC	42-43 consensus	(Z6)	428	TGCCCCAGGTATGGCATGGGACATGATGAACTGGAGTCCCACAAACCCTTGTTCC																
43	Z7	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG																		
42	Z6	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	428	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG																		
42-43 consensus	(Z6)	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	42-43 consensus	(Z6)	TGCCCCAGGTATGGCATGGCAGCTGGTGGACTCTGGTGGACTCTGGCACTGGGACTCTGGG	42-43 consensus	(Z6)	489	TatCCTTAatCgggttGGCatACTTCTGCATGCAAGCTAAATTGGCCAAGCTCATCTGGTC	42-43 consensus	(Z6)	489	CgtCCTTGTGGTGGGTGGCTACTTCAGtATGCAGGCTAAATTGGCCAAGCTCATCTGGTC	42-43 consensus	(Z6)	489	CgtCCTTGTGGTGGGTGGCTACTTCAGtATGCAGGCTAAATTGGCCAAGCTCATCTGGTC	42-43 consensus	(Z6)	550	CTTTTCTCTTactCGCTGGAGTTGATGCC	42-43 consensus	(Z6)	550	CTTTTCTCTTCTCGCTGGAGTTGATGCC	42-43 consensus	(Z6)	550	CTTTTCTCTTCTCGCTGGAGTTGATGCC
43	Z7	550	CTTTTCTCTTactCGCTGGAGTTGATGCC	42	Z6	550	CTTTTCTCTTCTCGCTGGAGTTGATGCC	42-43 consensus	(Z6)	550	CTTTTCTCTTCTCGCTGGAGTTGATGCC																		

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FIGURE 1G-1

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	
47	SA5	
49	SA7	
46	SA4	
50	SA13	
48	SA6	
45-50	consensus	

1	GTTCCCTACCGgAAATGCCCTCTGGGTTTACCATGTCACCAATTGACTGCCAACCTGccTCCA	
1	GTCCTACCGAAATGCCCTGGGTTTATCATGTCAACATTGATTGCCAACACTTCCA	
1	GTCCTACCGAAATGCCCTGGGTTTATCATGTCAACATTGATTGCCGAACCTTCCA	
1	GTTCCCTACCGAAACGCCCTCTGGGTTTATCATGTCAACATTGATTGCCAACACTTCCA	
1	GTTCCCTACCGAAATGCCCTCTGGGTTTATCATGTCAACATTGATTGCCAACACTTCCA	
1	GTTCCCTACCGAAATGCCCTCTGGGTTTATCATGTCAACATTGATTGCCAACACTTCCA	
1	GTTCCCTACCGAAATGCCCTCTGGGTTTATCATGTCAACATTGATTGCCAACACTTCCA	
	GTTCCCTACCGAAAtGCCCTGGGTTTATCATGTCAACATTGATTGCCAACACTTCCA	
62	TAGTCTACGGGCTGATAACCTGATCTTGCACGGCCTGGCTGGCTGCCCTGTGTCAGGCA	
62	TAGTCTACGGGCTGATAACCTGATCTGCACGGCACCTGGCTGGCTGGCTGGCTAAAGGA	
62	TAGTCTATGGGCTGACAACCTGATCTGCACGGCACCTGGCTGGCTGGCTGGCTAGGCA	
62	TAGTtTAGGGCTGATAACCTGATCTTGCATGCACCTGGCTGGCTGGCTGGCTAGGCA	
62	TAGTtTAGGGCTGATAACCTGATCTTGCATGCACCTGGCTGGCTGGCTGGCTAGGCA	
62	TAGTCTACGGGCTGATGACCTGATCTTACAGGCAACCTGGCTGGCTGGCTGGCTAGGCA	
62	TAGTCTACGGGCTGATGACCTGATCTTACAGGCAACCTGGCTGGCTGGCTGGCTAGGCA	
62	TAGTCTACGGGCTGATGACCTGATCTTACAGGCAACCTGGCTGGCTGGCTGGCTAGGCA	
	TAGTCTACGGGCTGATAACCTGATCTTACAGGCAACCTGGCTGGCTGGCTGGCTAGGCA	

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FIGURE 1G-2

<u>SEQ_ID NO:</u>	<u>Isolate</u>	<u>SEQ_ID NO:</u>	<u>Isolate</u>
45	SA1	123	AGataATGTCAGTAGGTCTGGTCCAAATCACCCCCAACACTGTCAAGCCCCGACCTTCGGA
47	SA5	123	ACgTAATGTCAGTAGGTCTGGTCCAAATCACCCCCAACATTGTCAAGCCCCGAACCTCGGA
49	SA7	123	AaATAATGTCAGTAGGTCTGGTCCAAATCACCCCCAACATTGTCAAGCCCCGAACCTCGGA
46	SA4	123	AGATAATGTCAGTAAGTGCTGGTCAAATCACCCCCAACGTTGTCAGCCCCGAATCTCGGA
50	SA13	123	GggTAATGTCAGTAGGTCTGGTCCAGATCACCCCCAACACTGTCAAGCCCCGAGCCTCGGA
48	SA6	123	GGataATGTCAGTAGAtTGCTGGTTCAATCACCCCCAACATACTAGGCCCGAGCCTCGGA
45-50	consensus		agataATGTCAGTAGgtGCTGGTccAAATCACCCCCAAC - TgtCAAGCCCCGAAactCTCGGA
45	SA1	184	GCGGTCA CGGCT CCT TCGAAGGGc CGTTGACTACTTAGCGGGAGGGAGCTGCT
47	SA5	184	GCGGTCA CGGCT CCT TCGAAGGGt CGTTGACTACTTAGCGGGAGGGCTGCCCTCTGCT
49	SA7	184	GCGGTCA CGGCT CCT TCGAAGGGCTTGA CTACCTAGCGGGAGGGCTGCCCTCTGCT
46	SA4	184	GCGGTCA CGGCT CCT TCGAAGGGCTTGA CTACTTAGCGGGAGGGCTGCCCTCTGCT
50	SA13	184	GCGGTCA CGGCT CCT TCGAAGGGCTTGA CTACTTAGCGGGAGGGCTGCCCTCTGCT
48	SA6	184	GCGGTCA CGGCT CCT TCGAAGGGCTTGA ATCTTgCGGGAGGGCCGCCCTGTGCT
	consensus		

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FIGURE 1G-3

<u>SEQ ID NO:</u>	<u>Isolate</u>		<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1		45	CCGCACTATACTGTCCCCGACGGCGTGGGGCAGTGTt-ctGGTAGGCCAAATGGTCACCTA	245
47	SA5		47	CCGCACTATACTGTCCCCGACGGCGTGGGGCAGTGTt-ctGGTAGGCCAAATGGTCACCTA	245
49	SA7		49	CCGCGCTATACTGTCCCCGACGGCGTGGGGCAGTGTt-ctGGTAGGCCAAATGGTCACCTA	245
46	SA4		46	CCGCaCTATACTGTCCCCGACGGCGTGGGGCAGTGTt-ctGGTAGGCCAAATGGTCACCTA	245
50	SA13		50	CCGCGTTATACTGTCCCCGAGACGGCGTGGGGCAGTGTt-ctGGTAGGCCAAATGGTCACCTA	245
48	SA6		48	CCGCGTTATACTGTCCCCGAGACGGCGTGGGGCAGTGTt-ctGGTAGGCCAAATGGTCACCTA	245
45-50	consensus		45-50	CCGC-ctTATACGTCCCCGACGGCGTGGGGCAGTGTt-ctGGTAGGCCAAATGGTCACCTA	
45	SA1		306	TAGGCCCTGCCAGCATACCACactGGCAGACTGCAACTGTCATTACAGTGGCCATATC	
47	SA5		306	TAGGCCCTGCCAGCATACTACGGTGCAGGAAGTGCACACTGTCATTACAGGCGCCATATC	
49	SA7		306	TAGGCCCTGCCAGCACACTACGGTGCAGGAAGTGCACACTGTCATTACAGTGGCCATATC	
46	SA4		306	TAGGCCCTGCCAGCACACTACGGTGCACAGTGCACACTGTCATTACAGTGGCCATATC	
50	SA13		306	TAGGCCCTGCCAGCATTAatggttGTGCAGGAAGTGCACACTGTCATTACAGTGGCCACATC	
48	SA6		306	TAGGCCCTGCCAGCATAcggACTGCAACTGTCATTACAGTGGCCATATC	
45-50	consensus		45-50	TAGGCCCTGCCAGCATactacgtggCAggACTGCAACTGTCATTACAGTGGCCATATC	

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FIGURE 1G-4

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	
47	SA5	367 ACCGGCCACCGGATGGCATTGGGACATGGATGATGAATTGGTACCTACGACAGCCTTGCTGA
49	SA7	367 ACCGGCCACCGAATGGCATGGGACATGGATGATGAATTGGTACCTACGACAGCCTTGCTGA
46	SA4	367 ACCGGCCACCGGATGGCATGGGACATGGATGATGAATTGGTACCTACGACAGCCTTGCTGA
50	SA13	367 ACCGGCAACCGGATGGCATGGGACATGGATGATGAATTGGTACCTACaACAGCTTGCTGA
48	SA6	367 ACTGGCACCCGGATGGCATGGGACATGGATGATGAATTGGTACCCcgACAGCcTTGGTGA
45-50	consensus	ACGGGCCACCGGATGGGACATGGATGATGAATTGGTACCTAGCATGGCTTGCTGA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	428 TGGCCCAAGtACGGATCCCAAGGTGGTCATAAGACATATAAGCCGGGCCACTGGGG
47	SA5	428 TGGCCCAAGtGGCTACGGATTCCCAAGGTGGTCATGACATATTGCCGGGCCACTGGGG
49	SA7	428 TGGCCCAAGtGGCTACGGATTCCCAAGGTGGTCATGGACATATTGCCGGGCCACTGGGG
46	SA4	428 TGGCCCAAGtGGCTACGGATTCCCAAGGTGGTCATGGACATATTGCCGGGCCACTGGGG
50	SA13	428 TGGCCCAAGtGGCTACGGATTCCCAAGGTGGTCATTGACATATTGCCGGGCCACTGGGG
48	SA6	428 TGGCCCAAGtGGCTACGGATTCCCAAGGTGGTCATTGACATATTGCCGGGCCACTGGGG
45-50	consensus	TGGCCCAAGtTGtACGGATTCCCAAGGTGGTCATTGACATATTGCCGGGCCACTGGGG

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FIGURE 1G-5

<u>SEQ ID NO:</u>	<u>Isolate</u>		<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	489	45	SA1	550
47	SA5	489	47	SA5	550
49	SA7	489	49	SA7	550
46	SA4	489	46	SA4	550
50	SA13	489	50	SA13	550
48	SA6	489	48	SA6	550
45-50	consensus	GGTCTTGTTCGCCGCCATACttcGGC-GCGGtAACTGGGCTAAGGGTgtGTGGTC	45-50	consensus	-TGTTtCTGTTGGGGGTCCATGCC

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FIGURE 1H-1

<u>SEQ ID NO:</u>	<u>Genotype</u>						
30-33	(IV/2b)						
34	(2c)						
26-29	(III/2a)						
35-39	(V/3a)						
9-25	(II/1b)						
1-8	(I/1a)						
40	(4a)						
42-43	(4c)						
44	(4d)						
41	(4b)						
45-50	(5a)						
51	(6a)						
1-51	consensus	A	TA	AC	AA	GA	TG
<u>SEQ ID NO:</u>	<u>Genotype</u>						
30-33	(IV/2b)						
34	(2c)						
26-29	(III/2a)						
35-39	(V/3a)						
9-25	(II/1b)						
1-8	(I/1a)						
40	(4a)						
42-43	(4c)						
44	(4d)						
41	(4b)						
45-50	(5a)						
51	(6a)						
1-51	consensus	A	T	T	CA	CC	GG

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FIGURE 1H-2

<u>SEQ ID NO.:</u>	<u>Genotype</u>
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

TG TGC T C CC A T C

<u>SEQ ID NO.:</u>	<u>Genotype</u>
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

123	CAATGGCACCCCTGCGCTGGATAACAAGTgACACTAAATGTGGCTGTGAAACACCCGcGGC	123	CGCCAAACGTCCTCTCGATGTTGGGTGCCGGTACCGGCTAACTCTGCCATAAGTCAACCTGGC	123	GGAAAATaCatCTCGGTGGATACCGGtctCACCAAACGTTGCCGTGcAGGCCGGC	123	CGGcAAATACATCCACGTCGGTGGACACTACAGTGGCAGTCAGGTAAGTCGGGA	123	gaacAAActCTCCcgCTGCTGGGTaGGGCTcaCTCCACGCTGGGCTcaG	123	GggTaacGccCTGAGgtGGTTGGGTGGGAGGAAACGCCAgC	123	TGGGAAACACATOGCCGTTGCTGAGCCGGTGAACGGCTAACAGTGGCTGTCGACACC	123	tGGGAAATCAGTCACGGCTGCTGGGTGGCCCTTACTCCACCGTGGGGGTGCTTATCGGT	123	AGGGAAACAAAGTCTACATGCTGGGTGTTCTCACCCCCACCGTGGCTGGCAACATCTGAAT	123	GGAGAAATACTTCTCGCTGGGTGGCTGGGTGGCCCTTGACCCCCACTGTGGCGGCCCTATCCAAC	123	agataAATGTCAGTAGGTTGCTGGGTCCAaaATCACCCCCACatTGTCAGGCCCCGAAactCTGG	123	CGATGGTCCACCTGTTGGCATGCTGTGACCCCCACCTGGCCATACCAAAATGCTTCC		
184	GCactCTCACAAACCTGGAaCaCATgtTcGAcAtGATGGCAGGTACGGTCTGCT	184	GCTCTCACTAAGGGCCCTGGGACACATCGATATCGTGAATGTCGCTACGGTCTGCT	184	GCCCTCACGGAGGGCTTGGGACGCACTGACATGGGACCTTGATGTCGCTACGGTCTGCT	184	GCAACCACCGCTTGGATACTGCACTGCACTGCACTGCACTGCACTGCACTGCA	184	GTCCCCACLAAGCAAACTACGAGCCACGCTTGAGTCGATGTCGCTACATCGTGA	184	9TCCCCAGCAAGCTTGAGTCGATGTCGCTACATCGTGA	184	CCTCCCGCAAGCTTGAGTCGATGTCGCTACATCGTGA	184	GCTCCGCTTGAGTCGTTCCGGGAGACATGTGGACTTAATGTA	184	GtCCGCTTGAGTCCTCCGGAGACATGTGGACCTGATGTCGCTACTGtaTGCT	184	GCTCCGCTTGAGTCGTTGAGTCGATGTCGCTACATCGTGA	184	GCACCGTTAGTCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA	184	GGGGTCAACGGCTCCCTTGGAGGGGCTGAGCTACTGACTAATGTTGTT	184	ACGCCCCAACGGATTCCGAGGCAATGTTCTTGCGGGGCACTGTTGCT

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FIGURE 1H-3

<u>SEQ ID NO.:</u>	<u>Genotype</u>	1-51	consensus	C	T	TA	T	GG	GA	TG	GG	T	T	CA	T
30-33	(IV/2b)														
34	(2c)														
26-29	(III/2a)														
35-39	(V/3a)														
9-25	(II/1b)														
1-8	(I/1a)														
40	(4a)														
42-43	(4c)														
44	(4d)														
41	(4b)														
45-50	(5a)														
51	(6a)														
1-51	consensus														

<u>SEQ ID NO.:</u>	<u>Genotype</u>	306	ATGCCaGAAcCCaAACTTtACCCAaGAGTGCAACTGTTCATCTACCAAGGTCAATTC
30-33	(IV/2b)	306	GTGCCAACCAACCCATACTGGTTGTGCAAGAACTGGCAACTGTTCATCTACCAAGGTCAATTC
34	(2c)	306	CTCGCCGaaACccCACTGGTTGTGCAAGAACTGGCAACTGTTCATCTACCAAGGTCAATTC
26-29	(III/2a)	306	CAGACCTCGTGCCTCATCAAACGGTCCAGACCTGTAACTGTGCTGCTGACCCAGGCCATCT
35-39	(V/3a)	306	306 CTICGCCCTGGCggCATggAGCAGttAGGACTGCAACTGTGCAAACTCTATCCGGGccacgta
9-25	(II/1b)	306	306 CTCTCCCAGGCGCCaaCTGGACaaACGCAAGACTGCAAACTGTGCAATTGGTTCAATCTATCCGGGccatata
1-8	(I/1a)	306	306 TCGGGCGGTGCCCCACTGGGACACTGGGAACTGGGAAATTGGTTCAATCTACTGGGccatata
40	(4a)	306	306 CAGCCGGAGCAGCCACTGGGACTACGGCAGACTGGGAAATTGGTTCAATCTACTGGGccatata
42-43	(4c)	306	306 CAAACCTGGCCCACTGGGAACTGGGAAATTGGTTCAATCTACTGGGccatata
44	(4d)	306	306 CGAACGGGGGGCACTGGGACACTGGGAAATTGGTTCAATCTACTGGGccatata
41	(4b)	306	306 TAGGCCCTGCCAGCATactacgtggACTGTGCAAGACTGCAACTGTGTCATCTCTGGTCACTGGTCACTGGTC
45-50	(5a)	306	306 TCAGCCCCGGCTCATGGGACTGTGCAAGACTGCAACTGTGTCATCTCTGGTCACTGGTCACTGGTC
51	(6a)		
1-51	consensus		

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FIGURE 1H-4

<u>SEQ_ID</u>	<u>ID NO.</u>	<u>Genotype</u>
30-33		(IV/2b)
34		(2c)
26-29		(III/2a)
35-39		(V/3a)
9-25		(II/1b)
1-8		(I/1a)
	40	(4a)
42-43		(4c)
44		(4d)
41		(4b)
45-50		(5a)
51		(6a)

consensus 1-51

<u>SEQ_ID</u>	<u>ID NO:</u>	<u>Genotype</u>
30-33		(IV/2b)
34		(2c)
26-29		(III/2a)
35-39		(V/3a)
9-25		(II/1b)
1-8		(I/1a)
	40	(4a)
	42-43	(4c)
	44	(4d)
	41	(4b)
	45-50	(5a)
	51	(6a)

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FIGURE 1H-5

<u>SEQ ID NO.:</u>	<u>Genotype</u>						
30-33	(IV/2b)						
34	(2c)						
26-29	(III/2a)						
35-39	(V/3a)						
9-25	(II/1b)						
1-8	(I/1a)						
40	(4a)						
42-43	(4c)						
44	(4d)						
41	(4b)						
45-50	(5a)						
51	(6a)						
1-51	consensus	T	T	G	GC	T	T
<u>SEQ ID NO.:</u>	<u>Genotype</u>	TGG	AA	GT	T		
30-33	(IV/2b)						
34	(2c)						
26-29	(III/2a)						
35-39	(V/3a)						
9-25	(II/1b)						
1-8	(I/1a)						
40	(4a)						
42-43	(4c)						
44	(4d)						
41	(4b)						
45-50	(5a)						
51	(6a)						
1-51	consensus	T	T	C	GG	GT	GA

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FIGURE 2A-1

<u>SEQ_ID NO:</u>	<u>Isolate</u>		<u>SEQ_ID NO:</u>	<u>Isolate</u>	
56	S14	1 YQVRNSTGLYHVTNDCPNSSIVYEaADAI.LH-PGCVPVCVREGnAsRCWVAMTPTVATRDGK	56	S14	62 LPatQLRRYIDLIVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRLWTTQdCNCSIYPGHI
52	DK7	1 YQVRNSTGLYHVTNDCPNSSIVYEaADAI.LH-TPGCCVFCVREGnS.RCWTAMTPTVATRDGK	52	DK7	62 LPTaQLRRHIDLIVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTOGNCNSIYPGHI
59	US11	1 YQVRNSTGLYHVTNDCPNSSIVYEaADAI.LH-TPGCCVFCVREGnAsRCWTAMTPTVATRDGK	59	US11	62 LPTTQLRRHIDLIVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTOGNCNSIYPGHI
55	DR4	1 HQVRNSTGLYHVTNDCPNSSIVYEaADAI.LH-TPGCCVFCVREGnS.RCWTAMTPTVATRDGK	55	DR4	62 LPTTQLRRHIDLIVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTOGNCNSIYPGHI
54	DR1	1 HQVRNSTGLYHVTNDCPNSSIVYEaADAI.LH-PGCVPVCVREGnAsRCWTAMTPTVATRDGK	54	DR1	62 LPTTQLRRHIDLIVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTOGNCNSIYPGHI
53	DK9	1 YQVRNSTGLYHVTNDCPNSSIVYEaADAI.LH-HSPGCVPCVREGnASKCWVAVAPTVATRDGK	53	DK9	62 LPATQLRRHIDLIVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTOGNCNSIYPGHI
58	SW1	1 YQVRNSTGLYHVTNDCPNSSIVYEaADAI.LH-HSPGCVPCVREGnASKCWVAVAPTVATRDGK	58	SW1	62 LPATQLRRHIDLIVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTOGNCNSIYPGHI
57	S18	1 YQVRNSTGLYHVTNDCPNSSIVYEaADAI.LH-HSPGCVPCVREGnAsRCWVAVAPTVATRDGK	57	S18	62 LPATQLRRHIDLIVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTOGNCNSIYPGHI
52-59	consensus	YQVRNSTGLYHVTNDCPNSSIVYEaADAI.LH - PGCVPCVREGnAsRCWVAVAPTVATRDGK	52-59	consensus	LP-tQLRRHIDLIVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRhtWTTQdCNCSIYPGHI

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FIGURE 2A-2

<u>SEQ ID NO.:</u>	<u>Isolate</u>		<u>SEQ ID NO.:</u>	<u>Isolate</u>	
56	S14		56	S14	184 LLLFAGVDA
52	DK7	123 TGHRMAWDMMMNWSPTTALVVAQQLRIPQAILEDMIAGAHWGVLAGIAYFSMVGNGWAKVLV	52	DK7	184 LLLFAGVDA
59	US11	123 TGHRMAWDMMMNWSPTTAALVVAQQLRIPQAILEDMIAGAHWGVLAGIAYFSMVGNGWAKVLV	59	US11	184 LLLFAGVDA
55	DR4	123 TGHRMAWDMMMNWSPTTALVVAQQLRIPQAILEDMIAGAHWGVLAGIAYFSMVGNGWAKVLV	55	DR4	184 LLLFAGVDA
54	DR1	123 TGHRMAWDMMMNWSPTTAALVVAQQLRIPQAILEDMIAGAHWGVLAGIAYFSMVGNGWAKVLV	54	DR1	184 LLLFAGVDA
53	DK9	123 TGHRMAWDMMMNWSPTTALVMAQQLRIPQAILEDMIAGAHWGVLAGIAYFSMVGNGWAKVVV	53	DK9	184 LLLFAGVDA
58	SW1	123 TGHRMAWDMMMNWSPTTALVVAQQLRIPQAVIDLMIAGAHWGVLAGIAYFSMVGNGWAKVLV	58	SW1	184 LLLFAGVDA
57	S18	123 TGHRMAWDMMMNWSPTTALVIAQQLRvPQAVLDIAGAHWGVLAGIAYFSMAGNGWAKVLV	57	S18	184 LLLFAGVDA
52-59	consensus	TGHRMAWDMMMNWSPTTALVVAQQLRIPQAILEDMIAGAHWGVLAGIAYFSMVGNGWAKVLV	52-59	consensus	LLLFAgVDA

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FIGURE 2B-1

SEQ ID NO:	Isolate	T10	1	YEVNVSGmYHVTNDCSNSIVFEaaD1IMHTPGCVPVCREGNSSRCWVALTPTLAARNs
62	DK1	1	1	YEVNVSGvYHVTNDCSNSIVYEAvD1IMHTPGCVPVCRENhSRCWVALTPTLAARNs
64	HK4	1	1	heVNvSGiYHVTNDCSNSIVYEADM1MHTPGCVPVCRENNSRCWVALTPTLAARNs
76	US6	1	1	YEVNVSGmYHVTNDCSNSIVYEADM1MHTPGCVPVCRENNSRCWVALTPTLAARNs
68	IND8	1	1	YEVNVSGvYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSCWVALTPTLAARNs
67	IND5	1	1	YEVNVSGvYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
73	SW2	1	1	YEVNVSGvYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
63	HK3	1	1	YEVNVSGiYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
66	HK8	1	1	YEVNVSGiYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
61	D3	1	1	YEVNVSGvYQTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
74	T3	1	1	YEVNVSGvYVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
65	HK5	1	1	YEVNVSGvYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
71	S45	1	1	YEVNVSGaYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
72	SA10	1	1	YEVNVSGmYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
69	P10	1	1	YEVNVSGvYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNs
60	D1	1	1	YEVNVSGvYHVTNDCSNSIVYEADM1MHTPGCVPVCREGNfSSRCWVALTPTLAARNg
70	S9	1	1	YEVNVSGvYHVTNDCSNSIVYEaAdVIMHTPGCVPVCqEGNSSqCWVALTPTLAARNat
	consensus			yEVNVSGvYHVTNDCSNSIVYEaaD1mHtPGCVPcvEnNsSrCwVALTPTLAARNs

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FIGURE 2B-2

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
75	T10	
62	DK1	62 VPTTTTIRRHV DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET 1 QD NC CS IYP GHV
64	HK4	62 IPTTTI RRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET a QD NC CS IYP GHV
76	US6	62 IPTTTI RRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v QD NC CS IYP GHV
68	IND8	62 VPTTTI RRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET q QD NC CS IYP GHV
67	IND5	62 VPTTTI RRh HV DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v QD NC CS IYP GHV
73	SW2	62 VPTTTI RRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v QD NC CS IYP GHV
63	HK3	62 VPTTTI RRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v QD NC CS IYP GHV
66	HK8	62 VPTTTI RRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v Qe C NC CS IYP GHV
61	D3	62 VPTTTI RRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v Qe C NC CS IYP GHV
74	T3	62 VPTK TIRRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v QD NC CS IYP GHV
65	HK5	62 VPTTA IRRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v QD NC CS IYP GHV
71	S45	62 VPTTTI RRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v QD NC CS IYP GHV
72	SA10	62 VPTTTI RRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v QD NC CS IYP GHV
69	P10	62 VPTTA IRRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v QD NC CS IYP GHV
60	D1	62 VPTTA IRRH V DLLVGA AAA AFC SAM YVG DL CG SV FLY SQL FT FSP RR HET v Qe C NC CS IYP GHV
70	S9	62 VPTTTI RRH V DLLVGA AVFCS AM YVG DL CG SV FLY SQL FT FSP RR HET v Qn NC CS IYP GHV
60-76	consensus	VPTttI RRH V DLLVGA Aa FC SA M YVG DL CG SV FLY SQL FT FSP RR h e r v Qd NC CS IYP GHv

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FIGURE 2B-3

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	123 SGHMAWDMMMNWSPTTALVVSQQLRIPQAVmDMVtGAHWGVLAGLAYSMAGNWA KV LIV
62	DK1	123 SGHMAWDMMMNWSPTTALV1SQLLRIPQA VvDMVAGAHWGVLAGLAYSMAGNWA KV LIV
64	HK4	123 SGHMAWDMMMNWSPTAALVVSQQLR1PQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
76	US6	123 SGHMAWDMMMNWSPTAALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
68	IND8	123 SGHMAWDMMMNWSPTAALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
67	IND5	123 SGHMAWDMMMNWSPTAALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
73	SW2	123 SGHMAWDMMMNWSPTAALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
63	HK3	123 SGHMAWDMMMNWSPTAALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
66	HK8	123 SGHMAWDMMMNWSPTTALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
61	D3	123 TGHMAWDMMMNWSPTaALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
74	T3	123 TGHMAWDMMMNWSPTTALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
65	HK5	123 TGHMAWDMMMNWSPTTALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
71	S45	123 TGHMAWDMMMNWSPTaALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
72	SA10	123 TGHMAWDMMMNWSPTTALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
69	P10	123 SGHMAWDMMMNWSPTaALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
60	D1	123 TGHMAWDMMMNWSPTTALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
70	S9	123 TGHMAWDMMMNWSPTTALVVSQQLRIPQA VMDMVAGAHWGVLAGLAYSMAGNWA KV LIV
		SGHMAWDMMMNWSPTaALVVSQQLRIPQA VvDMVAGAHWGVLAGLAYSMAGNWA KV LIV
		consensus

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FIGURE 2B-4

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	184 mLLFAGVDG
62	DK1	184 lLlFAGVDG
64	HK4	184 mLLFAGVDG
76	US6	184 lLLFAGVDG
68	IND8	184 mLLFAGVDG
67	IND5	184 mLLFAGVDG
73	SW2	184 mLLFAGVDG
63	HK3	184 mLLFAGVDG
66	HK8	184 mLLFAGVDG
61	D3	184 mLLFAGVDG
74	T3	184 lLLFAGVDG
65	HK5	184 mLLFAGVDG
71	S45	184 mLLFAGVDG
72	SA10	184 mLLFAGVDG
69	P10	184 mLLFAGVDG
60	D1	184 mLLFAGVDG
70	S9	184 mLLFAGVDG
60-76	consensus	mLLFAGVDG

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FIGURE 2C-1

<u>SEQ ID NO.:</u>	<u>Isolate</u>		
77	T2	1	AQVrNTsrgYMTNDCSNeSITWQLQAAVLHVPGCIPCErlGNtSRCWIPVtPNVAVRQPG
78	T4	1	AQVKNTnSYMTNDCSNDSITWQLQAAVLHVPGCVPCEktGNtSRCWIPVSPNVAVRQPG
79	T9	1	AevKNTSTSsYMTNDCSNDSITWQLQAAVLHVPGCVPCErVGNAsrcWIPVSPNVAVQRPG
80	US10	1	vqVKNTSTSsYMTNDCSNDSITWQLQAAVLHVPGCVPCEkVGNtSRCWIPVSPNVAVQRPG
77-80	consensus		aqVKNTstsYMTNDCSNDSITWQLqAAVLHVPGCvPCE-vGNTsrcWIPVSPNVAV--PG
<u>SEQ ID NO.:</u>	<u>Isolate</u>		
77	T2	62	ALTQGLRTHIDMvVMSATLCSALYVGDLCGGVMLAAQMFIvSPrrHWFVQeCNCSIYPGTI
78	T4	62	ALTQGLRTHIDMvVMSATLCSALYVGDLCGGVMLAAQMFIvSPQHHWFVQdCNCSIYPGTI
79	T9	62	ALTQGLRTHIDMvVMSATLCSALYVGDLCGGVMLAAQMFIvSPQHHWFVQeCNCSIYPGTI
80	US10	62	ALTQGLRTHIDMvVMSATLCSALYVGDLCGGVMLAAQMFIvSPRHsFVQeCNCSIYPGTI
77-80	consensus		ALTQGLRTHIDMvVMSATLCSALYVGDLCGGVMLAAQMFIvSP-hHWFVQeCNCSIYPGTI
<u>SEQ ID NO.:</u>	<u>Isolate</u>		
77	T2	123	TGHRMAWDMMNNWSPTATMILAYAMRVPEVIdIiGAHWGVmFGLAYFSM0GAWAKVVI
78	T4	123	TGHRMAWDMMNNWSPTATMILAYAMRVPEVIdIVSGAHWGVMFGLAYFSM0GAWAKVVVI
79	T9	123	TGHRMAWDMMNNWSPTtTMILAYAMRVPEVIdIISGAHWGVmFGLAYFSM0GAWAKVVVI
80	US10	123	TGHRMAWDMMNNWSPTat1IIAYvMRVPEVIdIISGAHWGV1FGLAYFSM0GAWAKVVVI
77-80	consensus		TGHRMAWDMMNNWSPTatMILAYAMRVPEVIdIisGAHWGVmFGLAYFSM0GAWAKVVVI

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FIGURE 2C-2

<u>SEQ_ID NO:</u>	<u>Isolate</u>	
77	T2	184 LLLAAGVDA
78	T4	184 LLLAAGVDA
79	T9	184 LLLtAGVDA
80	US10	184 LLLaAGVDA
77-80	consensus	LLLaAGVDA

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FIGURE 2D-1

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
82	DK11	
83	SW3	
84	T8	
81	DK8	
81-84	consensus	

VEVRN-SSYYATNDCSNN.SITWQQLNAVHLPGCVPCENDNGTL-CWIQVTPNVAVKHRC

<u>SEQ_ID NO.:</u>	<u>Isolate</u>	<u>DK11</u>	<u>SN3</u>	<u>T8</u>	<u>DK8</u>	<u>consensus</u>
82						
83						
84						
81						
	81-84					

ALTHNLR-HVD-IVMAATVCSALLYGBDVGGAIVSOAFLISPERHETEOFCCNCSLYOGLI

<u>SEQ ID NO.:</u>	<u>Isolate</u>
82	DK11
83	SW3
84	T8
81	DK8
81-84	consensus

TGHRMAWDMMLNWSPTLTMILAYAARVPELVLEWVFGGHGVVFGLAYFSMOGAWAI

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FIGURE 2D-2

<u>SEQ ID NO:</u>	<u>Isolate</u>
82	DK11
83	SW3
84	T8
81	DK8
81-84	consensus

184 LLLVAGVDA
184 LLLVAGVDA
184 LLLVAGVDA
184 LLLVAGVDA
184 LLLVAGVDA

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FIGURE 2E-1

<u>SEQ ID NO:</u>	<u>Isolate</u>
86	DK12
87	HK10
88	S2
90	S54
89	S52
86-90	consensus

```

1 LEWRNVSGLYYVLTNDCSNSSIIVYEADDVILHTPGCVPVCQDGNTSTCWTSVTPVAVRYVG
1 LEWRNVSGLYYVLTNDCPNSSIIVYEADDVILHTPGCVPVCQDGNTSTCWTSVTPVAVRYVG
1 LEWRNTSGLYLITNDCSNSSIIVYEADDVILHTPGCVPVCQDGNTSTCWTPVTPVAVRYVG
1 LEWRNTSGLYLITNDCSNSSIIVYEADDVILHTPGCVPVCQDGNTSTCWTPVTPVAVRYVG
1 LEWRNTSGLYLITNDCSNSSIIVYEADDVILHTPGCVPVCQDGNTSmCWTPVTPVAVRYVG

```

LEWRNTSGLYLITNDCSNSSIIVYEADDVILHTPGCVPVCQDGNTS_tCWTPVTPVAVRYVG

<u>SEQ ID NO:</u>	<u>Isolate</u>
86	DK12
87	HK10
88	S2
90	S54
89	S52
86-90	consensus

```

62 ATTASIRSHVDLLVGAATMCSALYVGDFCGAFLYGOAFTERPRRRHOTVQTNCNSLYPGHL
62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAFLYGOAFTFPRRHOTVQTNCNSLYPGHL
62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAFLYGOAFTFPRRHOTVQTNCNSLYPGHL
62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAFLYGOAFTFPRRHOTVQTNCNSLYPGHL
62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAFLYGOAFTFPRRHOTVQTNCNSLYPGHL

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ATTASIRSHVDLLVGAATMCSALYVGDMCGAFLYGOAFTFPRRHOTVQTNCNSLYPGHL

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FIGURE 2E-2

<u>SEQ ID NO:</u>	<u>Isolate</u>		<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	123 SGHRAWDMMNNWSPAVGMVVVAHVLRLLPQTTLFDI IAGAHWGIAGLAYYSMQGNWAKVAI	86	DK12	184 MVMFSGVDA
87	HK10	123 SGHRAWDMMNNWSPAVGMVVVAHVLRLLPQTTLFDI IAGAHWGIAGLAYYSMQGNWAKVAI	87	HK10	184 MVMFSGVDA
88	S2	123 SGHRAWDMMNNWSPAVGMVVVAHVLRLLPQTTLFDI IAGAHWGIAGLAYYSMQGNWAKVAI	88	S2	184 MVMFSGVDA
90	S54	123 SGHRAWDMMNNWSPAVGMVVVAHVLRLLPQTTLFDI IAGAHWGIAGLAYYSMQGNWAKVAI	90	S54	184 MIMFSGVDA
89	S52	123 SGHRAWDMMNNWSPAVGMVVVAHVLRLLPQTTLFDI IAGAHWGIAGLAYYSMQGNWAKVAI	89	S52	184 MIMFSGVDA
86 - 90	consensus	SGHRAWDMMNNWSPAVGMVVVAHVLRLLPQTTLFDI IAGAHWGIAGLAYYSMQGNWAKVAI	86 - 90	consensus	MVMFSGVDA

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FIGURE 2F

<u>SEQ ID NO:</u>	<u>Isolate</u>		
94	Z7	1	VNYhNASGVYHiTNDCPNSSImYEAEHHILHLPGCCVReGNQSRCWVALTPPTVAAPYIG
93	Z6	1	VNYRNASGVYHVTNDCPNSSIVYEAEHqILHLPGC1PCVRvgNQSRCWVALTPPTVAVsYIG
93-94 consensus (Z6)			VNYrRNASGVYHVTNDCPNSSIVYEAEHqILHLPGCL1PCVRvgNQSRCWVALTPPTVAVsYIG
<u>SEQ ID NO:</u>	<u>Isolate</u>		
94	Z7	62	APLESiRRHVDLiMVGAAATVCSALYiGDLGGVFVLYGOMFSFOPRRHWTtQDCNCStIYAGHV
93	Z6	62	APLdSLRRHVDLiMVGAAATVCSALYvGDLGGaFLVQOMFSFOPPRRHWTtQDCNCStIYAGHI
93-94 consensus (Z6)			APLdS1RRHVDLiMVGAAATVCSALYvGDLGGaFLVQOMFSFOPPRRHWTtQDCNCStIYAGHI
<u>SEQ ID NO:</u>	<u>Isolate</u>		
94	Z7	123	TGHRMAWDMMMNWSPTTTLLAQVMRIPSTLVLDLITGGHWGiliGvAYfcmQANWAKVILV
93	Z6	123	TGHRMAWDMMMNWSPTTTLLAQVMRIPSTLVLDLITGGHWGvLVGLAYfsmQANWAKVILV
93-94 consensus (Z6)			TGHRMAWDMMMNWSPTTTLLAQVMRIPSTLVLDLlaGGHWGvLvGLAYfsmQANWAKVILV
<u>SEQ ID NO:</u>	<u>Isolate</u>		
94	Z7	184	LFLYAGVDA
93	Z6	184	LFLFAGVDA
93-94 consensus (Z6)			LFLfAGVDA

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FIGURE 2G-1

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	
100	SA7	
97	SA4	
96	SA1	
99	SA6	
101	SA13	
96-101	consensus	
		VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVkegnvsrcmwQITPTLSAPnLG
		1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVQnVsrcwQITPTLSAPnLG
		1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQDNVSKCwQITPTLSAPnLG
		1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQDNVSKCwQITPTLSAPnLG
		1 VPYRNASGVYHVTNDCPNSSIVYEADSLILHAPGCVPCVRQDNVsrcwQITPTLSAPtFG
		1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRkDNVsrcwHITPTLSAPS LG
		1 VPYRNASGVYHVTNDCPNSSIVYEADDLILHAPGCVPCVRqgnvsrcwqITPTLSAPS LG
		VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVrqdnvsrcwvqITPTLSAPnLG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	
100	SA7	
97	SA4	
96	SA1	
99	SA6	
101	SA13	
96-101	consensus	
		AVTAPLRRavDYLAGGAALCSALyVGDAcGAVFLVGOMFTYRPRQHttVQDCNCSIYSGHI
		62 AVTAPLRRavDYLAGGAALCSALyVGDAcGAVFLVGOMFTYRPRQHttVQDCNCSIYSGHI
		62 AVTAPLRRavDYLAGGAALCSALyVGDAcGAVFLVGOMFTYRPRQHttVQDCNCSIYSGHI
		62 AVTAPLRRavDYLAGGAALCSALyVGDAcGAVFLVGOMFTYRPRQHttVQDCNCSIYSGHI
		62 AVTAPLRRavDYLAGGAALCSALyVGDAcGAVFLVGOMFTYRPRQHttVQDCNCSIYSGHI
		62 AVTAPLRRavDYLAGGAALCSALyVGDAcGAVFLVGOMFTYRPRQHttVQDCNCSIYSGHI
		62 AVTAPLRRavDYLAGGAALCSALyVGDAcGAVFLVGOMFTYRPRQHttVQDCNCSIYSGHI
		AVTAPLRRavDYLAGGAALCSALyVGDAcGAVFLVGOMFTYSPRrHnvQDCNCSIYSGHI

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FIGURE 2G-2

<u>SEQ ID NO.:</u>	<u>Isolate</u>		<u>SEQ ID NO.:</u>	<u>Isolate</u>	
98	SA5		98	SA5	184 LFLFAGVDg
100	SA7		100	SA7	184 LFLFAGVDA
97	SA4		97	SA4	184 LFLFAGVDA
96	SA1		96	SA1	184 LFLFAGVDg
99	SA6		99	SA6	184 LFLFAGVDA
101	SA13		101	SA13	184 LFLFAGVDA
96-101	consensus	TGHRM A WDMMNNWSPTTALVMAQvLRIPQVVIDIIAGGHWGVLF FAAYFASAANWAKVVLV	96-101	consensus	LFLFAGVDA

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FIGURE 2H-1

<u>SEQ ID NO:</u>	<u>Genotype</u>
81-84	(IV/2b)
85	(2c)
77-80	(III/2a)
86-90	(V/3a)
60-76	(II/1b)
52-59	(I/1a)
91	(4a)
93-94	(4c)
95	(4d)
92	(4b)
96-101	(5a)
102	(6a)
52-102	consensus
<u>SEQ ID NO:</u>	<u>Genotype</u>
81-84	(IV/2b)
85	(2c)
77-80	(III/2a)
86-90	(V/3a)
60-76	(II/1b)
52-59	(I/1a)
91	(4a)
93-94	(4c)
95	(4d)
92	(4b)
996-101	(5a)
102	(6a)
52-102	consensus

FIGURE 2H-1

	Y	TND	C	N	S	H	P	G	C	P	CW	CW	P
1	VEVRNISSEYYATNDCSNS	SITWQLTNAVLLP	GCVPCENDNGTL	rCWIQVT	PNVAVK	KRG							
1	VEVKDTGDSYMP	TNDCSN	SSIIWVOLEGA	VLLHTPG	CVP	CERTAN	VSR	CWV	VPA	NLAI	SPQG		
1	aqvkNTs	sSYMVT	NDCSN	dsITWQL	QAAVL	LHVPG	CY	PCE	KVGNT	LSRCW	I	SPQG	
1	LEWRNT	SGLYVLT	NDCSN	ssIVY	EADDV	LHTPG	CY	QDGN	T	CWTP	PTV	AVRYVG	
1	YEVrNVS	GvYh	VNTDCSN	ssIVY	Eaad	DmIm	HTPG	CvPCv	Regna	src	CWV	avt	PTVATRDGK
1	QVRNST	GLYH	VNTDCSN	ssIVY	Eaad	IlLhs	SPG	CV	MGTNTS	RC	CWTP	PTVAVAHPG	
1	EHYRNAS	GIYH	ITNDCP	PNSSIVY	eadH	HILHLP	GCV	PCV	MGTNTS	RC	CWTP	PTVAVAHPG	
1	VNYFNA	SGVYH	VNTDCSN	ssIVY	eaEHq	IlLHPG	C	CV	REGN	KST	CWV	SLTPTV	AQHLN
1	YNYRNSS	SGVYH	VNTDCSN	ssIVY	etDyH	IlLHPG	C	CV	REGN	KST	CWV	SLTPTV	AQHLN
1	WHYRNAS	SGVYH	VNTDCSN	ssIVY	etEHIM	HILHPG	C	CV	REGN	KST	CWV	SLTPTV	AQHLN
1	VPYRNAS	SGVYH	VNTDCSN	ssIVY	eadN	LILHAPG	C	CV	REGN	KST	CWV	SLTPTL	SAPn1G
1	LTYGNSS	GLYH	VNTDCSN	ssIVY	eadAM	ILHLPG	C	CV	REGN	KST	CWV	SLTPTL	AIPNAs

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FIGURE 2H-2

<u>SEQ ID NO.:</u>	<u>Genotype</u>	Deduced Amino Acid Sequence				
81-84	(IV/2b)	VVFGGHGVFGLAYFSMQGAWAKVIAI				
85	(2c)	TGHRMAWDMMNLNWSPPTLMILAYAARVPELVLeVVFGGHGVFGLAYFSMQGAWAKVIVI				
77-80	(III/2a)	TGHRMAWDMMMNWSPPTTMLAYLVRIPPEVILDIVTGGHGVFMGLAYFSMQGAWAKVVI				
86-90	(V/3a)	TGHRMAWDMMMNWSPPTAmlAYAMRVPEVIdIisGAHWGVmFGLAYFSMQGAWAKVvVI				
60-76	(II/1b)	SGRHMAWDMMMNWSPAVGMVVVAHVYLRLPQT1FDIiAGLAGYSSM0GNWAKVAlI				
52-59	(I/1a)	SGRHMAWDMMMNWSPTAalVV-SQOLLRIPOAVvDmVGAHMGVLAGLAYYSMvGNWAKVLIV				
91	(4a)	TGHRMAWDMMMNWSPTTALVVAAQLLRIPQAILDMIAGAHMGVLAGIAYFSMvGNWAKVlVV				
93-94	(4c)	TGHRMAWDMMMNWSPTTLLAQMVRPTAFLDMVAGGGHGVLAGLAYFSMQGNWAKVVLV				
95	(4d)	TGHRMAWDMMMNWSPTTLVLAQVMRIPSTLVDLLAGGGHGVLYGGLAYFSMQANWAKVILV				
92	(4b)	SGRHMAWDMMMNWSPTTLVLAQLMRIPGAMVLDLLAGGGHGVLYGIAYSMOSNWAkVILV				
96-101	(5a)	TGHRMAWDMMMNWSPTTALVMAQLRIPQVIDIAGGGHGVLFAAAYFASAANWAKVVLV				
102	(6a)	TGHRMAWDMMMNWSPTTLVLSSTLRVPEICASVIFGGHVGILLAVAYFGMAGNWLKVLA				
52-102	consensus	GHRMAWDMM NWSP	R P	G H W G	A	W KV
<u>SEQ ID NO.:</u>	<u>Genotype</u>	Deduced Amino Acid Sequence				
81-84	(IV/2b)	LLLIVAGVDA				
85	(2c)	184 LLLTAGVEA				
77-80	(III/2a)	184 LLLaAGVDA				
86-90	(V/3a)	184 MVMFSGVDA				
60-76	(II/1b)	184 mLFLFAGVDG				
52-59	(I/1a)	184 LLFLFAGVDA				
91	(4a)	184 LFLLFAGVDA				
93-94	(4c)	184 LFLLFAGVDA				
95	(4d)	184 LFLLFAGVDA				
92	(4b)	184 LFLLFAGVEG				
96-101	(5a)	184 LFLLFAGVDa				
102	(6a)	184 LFLLFAGVEA				
52-102	consensus	GV				

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FIGURE 3A

Genotype	SEQ ID NO:	Isolate	Sequence
IV/2b	DK11		VEVRNISSE-YA-S-n-ITWOLNAVL-L-V-EENDNGTLH--IQT-NVAVKRGALTHML-AH1-MIVHA-TV--AL-Y--Y--AVMIV
	SU3		VEVRNISSE-YA-S-s-ITWOLNAVL-L-V-EENDNGTLH--IQT-NVAVKRGALTHML-AH1-MIVHA-TV--AL-Y--Y--m--AVMIV
	DK8		VEVRNISSE-YA-S-n-ITWOLNAVL-L-V-EENDNGTLH--IQT-NVAVKRGALTHML-THV-VIVHA-TV--AL-Y--Y--v--AVMIV
	T8		VEVRNISSE-YA-S-h-ITWOLNAVL-L-V-EENDNGTLR--IQT-NVAVKRGALTHML-THV-VIVHA-TV--AL-Y--v--AVMIV
Zc	S8		VEVRNISSE-YD-S-ITWOLNAVL-S-S-ITWOLNAVL-V-EKIGTISR--IPV-NVAVPGALTGQI--THI-MVWMS-TL--AL-Y-f--GVMIA
	78	T4	ADVNTCTS-PV-S-D-ITWOLNAVL-V-EKIGTISR--IPV-NVAVPGALTGQI--THI-MVWMS-TL--AL-Y-f--GVMIA
	80	US10	ADVNTCTS-MV-S-D-ITWOLNAVL-V-EKIGTISR--IPV-NVAVPGALTGQI--THI-MVWMS-TL--AL-Y-f--GVMIA
	T9		ADVNTCTS-MV-S-D-ITWOLNAVL-V-EKIGTISR--IPV-NVAVPGALTGQI--THI-MVWMS-TL--AL-Y-f--GVMIA
	77	T2	ADVNTSTS-MV-S-e-ITWOLNAVL-V-EKIGTISR--IPV-NVAVPGALTGQI--THI-MVWMS-TL--AL-Y-f--GVMIA
(V)/3a	86	DK12	LETRNVSGL-VL-S-S-IVYEADVL-T-V-VGDEGTST--TSV-TVAVRVGATTAS--SHV-LLVGA-TH--AL-Y-H--AVFLV
	87	HK10	LETRNVSGL-VL-S-S-IVYEADVL-T-V-VGDEGTST--TSV-TVAVRVGATTAS--SHV-LLVGA-TH--AL-Y-N--AVFLV
	88	S2	LETRNVSGL-VL-S-S-IVYEADVL-T-V-VGDEGTST--TPV-TVAVRVGATTAS--SHV-LLVGA-TL--AL-Y-H--AVFLV
	90	S54	LETRNVSGL-IL-S-S-IVYEADVL-T-V-VGDEGTST--TPV-TVAVRVGATTAS--SHV-LLVGA-TL--AL-Y-H--AVFLV
	89	S52	LETRNVSGL-VL-S-S-IVYEADVL-T-V-VGDEGTSM--TPV-TVAVRVGATTAS--SHV-LLVGA-TL--AL-Y-H--AVFLV
	88	IND8	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	67	IND5	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	73	HK3	YEVRAVSGI-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	63	HK8	YEVRAVSGI-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	66	S45	YEVRAVSGS-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	71	D3	YEVRAVSGV-QW-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	74	T3	YEVRAVSGV-YV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	61	HK5	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	65	HK4	HEVRAVSGI-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	64	US6	YEVRAVSGI-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	76	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV	
	69	P10	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	72	SA10	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	75	T10	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	62	DK1	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	59	S9	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	70	D1	YEVRAVSGV-HV-S-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	52	DK7	YEVRAVSGI-HV-P-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	59	US11	YEVRAVSGI-HV-P-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	55	DR4	YEVRAVSGI-HV-P-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	54	DR1	YEVRAVSGI-HV-P-S-IVYEADVL-T-V-VREGASSR--VAL-TLAARIASVPTTTI-RHV-LLVGA-AF--AH-Y-L--SVFLV
	53	DK9	YEVRAVSGI-HV-P-S-IVYEADVL-T-S-V-VREGASK--VAVA-TVATRDGCLPATOL-RHI-LLVGS-TL--AL-Y--SVFLV
	58	SA1	YEVRAVSGI-HV-P-S-IVYEADVL-T-S-V-VREGASK--VAVA-TVATRDGCLPATOL-RHI-LLVGS-TL--AL-Y--SVFLV
	56	S14	YEVRAVSGI-HV-P-S-IVYEADVL-T-S-V-VREGASK--VAVA-TVATRDGCLPATOL-RHI-LLVGS-TL--AL-Y--SVFLV
	57	S18	YEVRAVSGI-HV-P-S-IVYEADVL-T-S-V-VREGASK--VAVA-TVATRDGCLPATOL-RHI-LLVGS-TL--AL-Y--SVFLV
	58	Z6	CHYRNASGV-HI-P-S-IVYEADVL-T-V-VREGASK--VAVA-TVATRDGCLPATOL-RHI-LLVGS-TL--AL-Y--SVFLV
	93	Z6	CHYRNASGV-HI-P-S-IVYEADVL-T-V-VREGASK--VAVA-TVATRDGCLPATOL-RHI-LLVGS-TL--AL-Y--SVFLV
	94	Z7	CHYRNASGV-HI-P-S-IVYEADVL-T-V-VREGASK--VAVA-TVATRDGCLPATOL-RHI-LLVGS-TL--AL-Y--SVFLV
	95	DK13	CHYRNASGV-HV-P-S-IVYEADVL-T-V-VREGASK--VAVA-TVATRDGCLPATOL-RHI-LLVGS-TL--AL-Y--SVFLV
	96	Z1	CHYRNASGV-HV-P-S-IVYEADVL-T-V-VREGASK--VAVA-TVATRDGCLPATOL-RHI-LLVGS-TL--AL-Y--SVFLV
I/1a	98	S15	CHYRNASGV-HV-P-S-IVYEADVL-T-A-V-VREGNSVR--VQI-TLSAPNLGAVTAPL-RHV-YLAGG-AL--AL-Y--Z-AVFLV
	100	SA7	CHYRNASGV-HV-P-S-IVYEADVL-A-V-VREGNSVR--VQI-TLSAPNLGAVTAPL-RHV-YLAGG-AL--AL-Y--A-AVFLV
	97	SA4	CHYRNASGV-HV-P-S-IVYEADVL-A-V-VREGNSVR--VQI-TLSAPNLGAVTAPL-RHV-YLAGG-AL--AL-Y--A-AVFLV
	98	SA1	CHYRNASGV-HV-P-S-IVYEADVL-A-V-VREGNSVR--VQI-TLSAPNLGAVTAPL-RHV-YLAGG-AL--AL-Y--A-AVFLV
	99	SA6	CHYRNASGV-HV-P-S-IVYEADVL-A-V-VREGNSVR--VQI-TLSAPNLGAVTAPL-RHV-YLAGG-AL--AL-Y--A-AVFLV
	101	SA13	CHYRNASGV-HV-P-S-IVYEADVL-A-V-VREGNSVR--VQI-TLSAPNLGAVTAPL-RHV-YLAGG-AL--AL-Y--A-AVFLV
	102	HK2	CHYRNASGV-HV-P-S-IVYEADVL-T-TGASSGV-HI-P-S-IVYEADVL-T-V-VREGNSVR--VQI-TLSAPNLGAVTAPL-RHV-YLAGG-AL--AL-Y--A-AVFLV

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FIGURE 3B

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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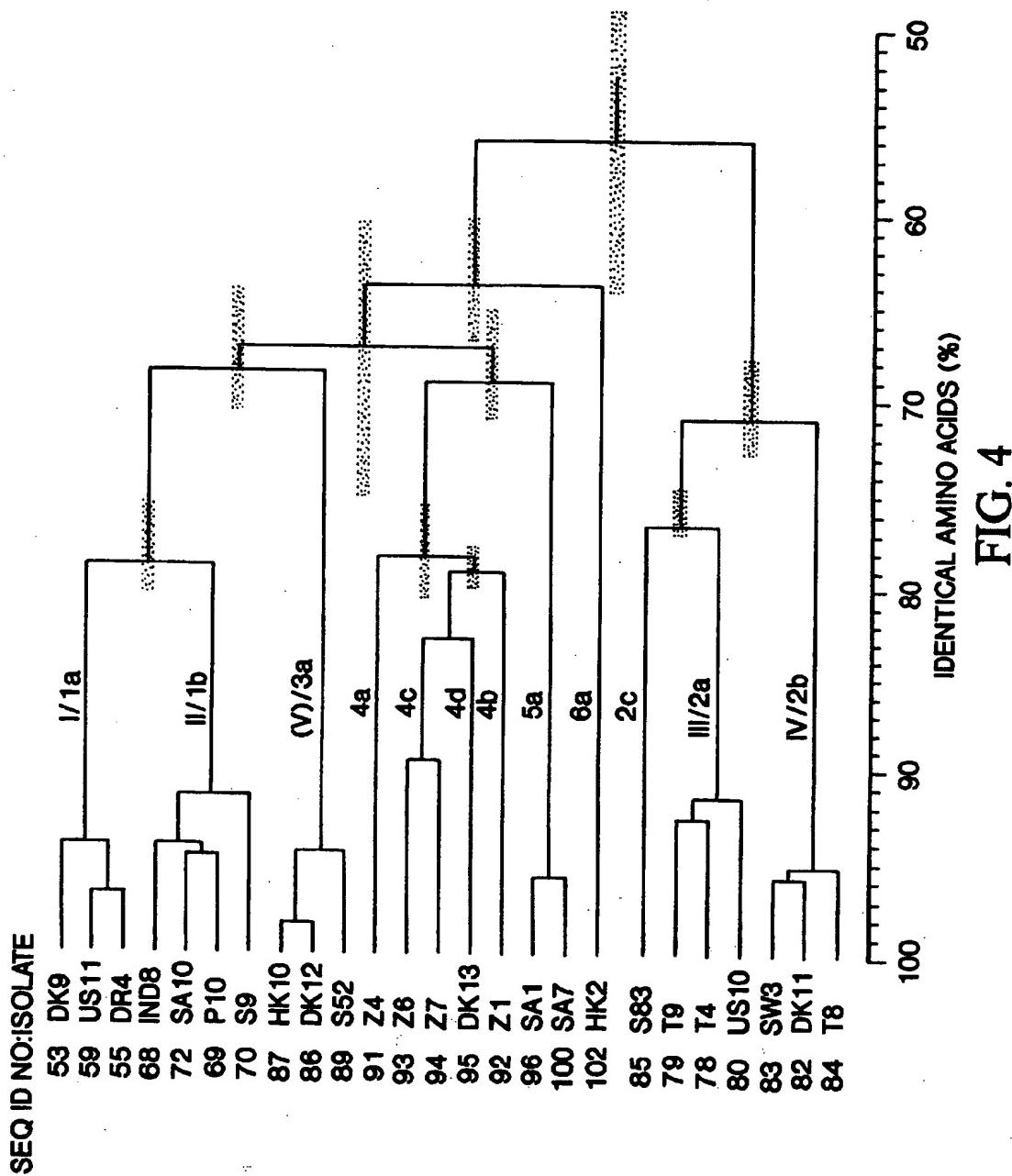


FIG. 4

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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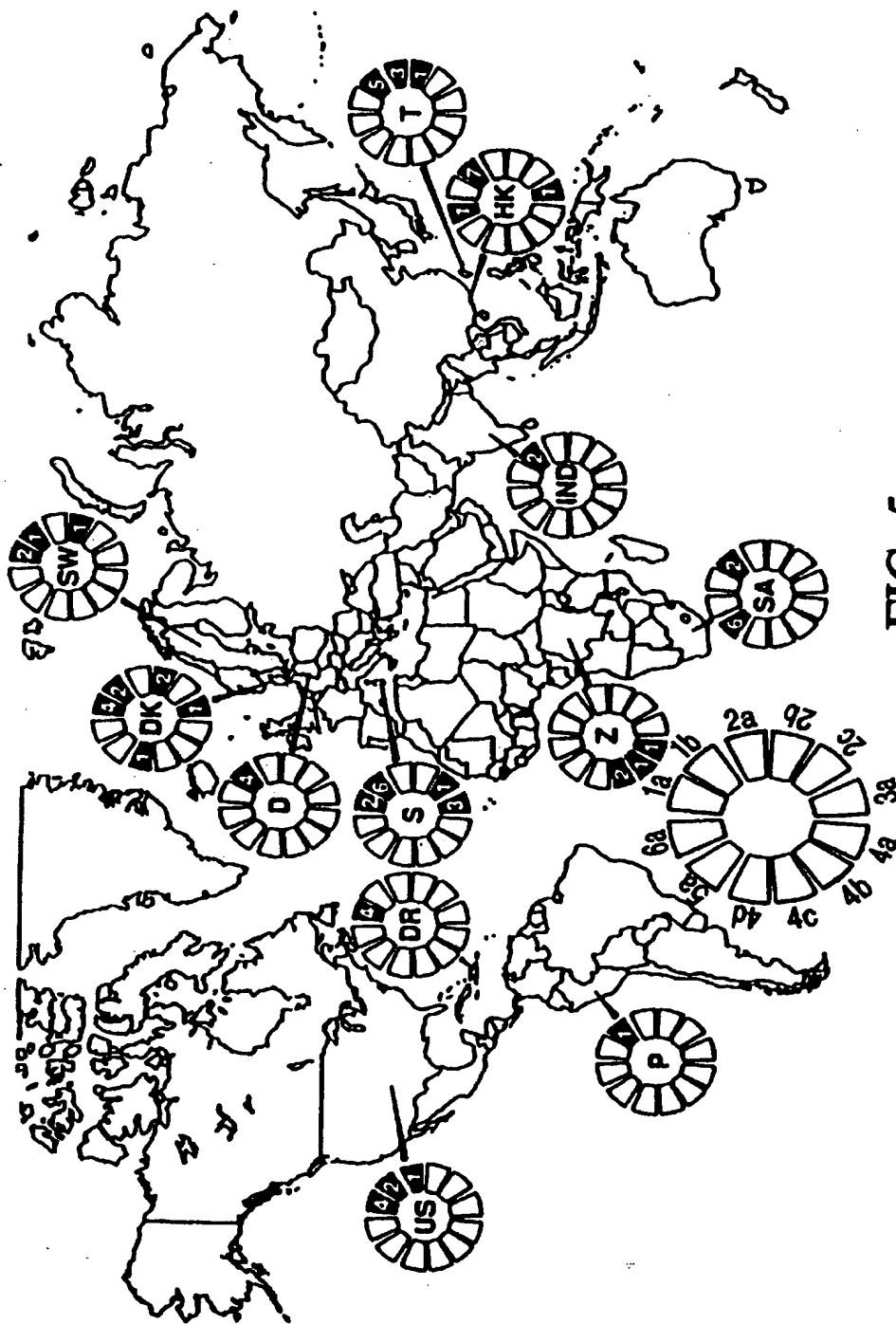


FIG. 5

**NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6A-1

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
108	DR4	1 ATGAGCACGAATCCTCAAAGAAAAACCAACCGTAACACCAACCGTGGCCACAGG
103	DK7	1 ATGAGCACGAATCCTCAAACCTCAAAGAAAAACCAACCGTAACACCAACCGTGGCCACAGG
104	US11	1 ATGAGCACGAATCCTCAAACCTCAAAGAAAAACCAACCGTAACACCAACCGTGGCCACAGG
105	S14	1 ATGAGCACGAATCCTCAAAGAAAAACCAACCGTAACACCAACCGTGGCCACAGG
106	SW1	1 ATGAGCACGAATCCTCAAAGAAAAACCAACCGTAACACCAACCGTGGCCACAGG
107	S18	1 ATGAGCACAAATCCTCAAAGAAAAACCAACCGTAACACCAACCGTGGCCACAGG
103-108	consensus	ATGAGCACGAATCCTCAAAGAAAAACCAACCGTAACACCAACCGTGGCCACAGG
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
108	DR4	62 ACGTCAAGTTCCGGGTGGGTCAAGATCGTTGGAGTTACTTGTGCCCCGGG
103	DK7	62 ACGTCAAGTTCCGGGTGGGTCAAGATCGTTGGAGTTACTTGTGCCCCGGG
104	US11	62 ACGTCAAGTTCCGGGTGGGTCAAGATCGTTGGAGTTACTTGTGCCCCGGG
105	S14	62 ACGTCAAGTTCCGGGTGGGTCAAGATCGTTGGAGTTACTTGTGCCCCGGG
106	SW1	62 ACGTCAAGTTCCGGGTGGGTCAAGATCGTTGGAGTTACTTGTGCCCCGGG
107	S18	62 ACGTCAAGTTCCGGGTGGGTCAAGATCGTTGGAGTTACTTGTGCCCCGGG
103-108	consensus	ACGTCAAGTTCCGGGTGGGTCAAGATCGTTGGAGTTACTTGTGCCCCGGG
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
108	DR4	123 CCCTAGATTGGGTGGCGGCCGAGAACCTTCGGGGTCGCAACCTCGAGGTAGA
103	DK7	123 CCCTAGATTGGGTGGCGGCCGAGAACCTTCGGGGTCGCAACCTCGAGGTAGA
104	US11	123 CCCTAGATTGGGTGGCGGCCGAGAACCTTCGGGGTCGCAACCTCGAGGTAGA
105	S14	123 CCCTAGATTGGGTGGCGGCCGAGAACCTTCGGGGTCGCAACCTCGAGGTAGA
106	SW1	123 CCCTAGATTGGGTGGCGGCCGAGAACCTTCGGGGTCGCAACCTCGAGGTAGA
107	S18	123 CCCTAGATTGGGTGGCGGCCGAGAACCTTCGGGGTCGCAACCTCGAGGTAGA
103-108	consensus	CCCTAGATTGGGTGGCGGCCGAGAACCTTCGGGGTCGCAACCTCGAGGTAGA

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FIGURE 6A-2

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>		
108	DR4	184 CGTCAGCCATATCCCAGGCqCGTCGGCCGAGGCCCTGGGTAC	
103	DK7	184 CGTCAGCCATATCCCAGGCACGTGGCCCGAGGCCCTGGGTAC	
104	US11	184 CGTCAGCCATATCCCAGGCACGTGGCCCGAGGCCCTGGGTAC	
105	S14	184 CGTCAGCCATATCCCAGGCACGTGGCCCGAGGCCCTGGGTAC	
106	SW1	184 CGTCAGCCATATCCCAGGCACGTGGCCCGAGGCCCTGGGTAC	
107	S18	184 CGTCAGCCATATCCCAGGCACGTGGCCCGAGGCCCTGGGTAC	
103-108	consensus	C GT C A G C C T A T C C C A A G G C - C G T C G G C C C A A G G C - C G T C G G C C C G A G G C A C C T G G G C T A G C C C G G T A C C	
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>		
108	DR4	245 CTTGGCCCCCTCATGGCAATGAGGGCTGGGGGTGGGGGATGGCTCCTGTCCCGTGG	
103	DK7	245 CTTGGCCCCCTCATGGCAATGAGGGCTGGGGGTGGGGGATGGCTCCTGTCCCGTGG	
104	US11	245 CTTGGCCCCCTCATGGCAATGAGGGCTGGGGGTGGGGGATGGCTCCTGTCCCGTGG	
105	S14	245 CTTGGCCCCCTCATGGCAATGAGGGCTGGGGGTGGGGGATGGCTCCTGTCCCGTGG	
106	SW1	245 CTTGGCCCCCTCATGGCAATGAGGGCTGGGGGATGGCTCCTGTCCCGTGG	
107	S18	245 CTTGGCCCCCTCATGGCAATGAGGGCTGGGGGATGGCTCCTGTCCCGTGG	
103-108	consensus	C TT G G C C C T C T A T G G C A A T G A G G G C T G G G G A T G G G G A T G G C T C C T G T C C C C G T G G	
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>		
108	DR4	306 CTCTCGGCCCTAGCTGGGCCAACAGACCCCCGGCGTAGGTGGCAATTGGTAAGGTC	
103	DK7	306 CTCTCGGCCCTAGCTGGGCCAACAGACCCCCGGCGTAGGTGGCAATTGGTAAGGTC	
104	US11	306 CTCTCGGCCCTAGCTGGGCCAACAGACCCCCGGCGTAGGTGGCAATTGGTAAGGTC	
105	S14	306 CTCTCGGCCCTAGCTGGGCCAACAGACCCCCGGCGTAGGTGGCAATTGGTAAGGTC	
106	SW1	306 CTCTCGGCCCTAGCTGGGCCAACAGACCCCCGGCGTAGGTGGCAATTGGTAAGGTC	
107	S18	306 CTCTCGGCCCTAGCTGGGCCAACAGACCCCCGGCGTAGGTGGCAATTGGTAAGGTC	
103-108	consensus	CTCTCGGCCCTAGCTGGGCCAACAGACCCCCGGCGTAGGTGGCAATTGGTAAGGTC	

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FIGURE 6A-3

<u>SEQ ID NO:</u>	<u>ISOLATE</u>		
108	DR4	367 ATCGACACCCTCACGGGCTTCGCCGACCTCATGGGTACATCCGGCTCGTGGGGCCC	
103	DK7	367 ATCGATAACCTTACGGGGCTTCGCCGACCTCATGGGTACATACCGCTCGTGGGGCCC	
104	US11	367 ATCCGATAACCTTACGGGGCTTCGCCGACCTCATGGGTACATACCGCTCGTGGGGCCC	
105	S14	367 ATCGATAACCTCACGGGCTTCGCCGACCTCATGGGTACATACCGCTCGTGGGGCCC	
106	SW1	367 ATCGATAACCTCACGGGCTTCGCCGACCTCATGGGTACATACCGCTCGTGGGGCCC	
107	S18	367 ATCGATAACCTCACGGGCTTCGCCGACCTCATGGGTACATACCGCTCGTGGGGCCC	
103-108	consensus	ATCGATAACCTCACGGGCTTCGCCGACCTCATGGGTACATACCGCTCGTGGGGCCC	
<u>SEQ ID NO:</u>	<u>ISOLATE</u>		
108	DR4	428 CcTTGGGGGCTGCCAGGGCCCTGGGCATGGGCTCCGAGTTCTGGAAAGACGGGGTGA	
103	DK7	428 CTCTTGGAAGGGCTGCCAGGGCCCTGGGCATGGGCTCCGGGTTCTGGAAAGACGGGGTGA	
104	US11	428 CTCCTGGAGGGGCGCTGCCAGGGCCCTGGGCATGGGCTCCGGGTTCTGGAAAGACGGGGTGA	
105	S14	428 CCCTCGGGGGGGCGCTGCCAGGGCCCTGGGCATGGGCTCCGGGTTCTGGAAAGACGGGGTGA	
106	SW1	428 CTCTGGAGGGGCGCTGCCAGGGCCCTGGGCATGGGCTCCGGGTTCTGGAAAGACGGGGTGA	
107	S18	428 CTCTCGGGGGGCGCTGCCAGGGCCCTGGGCATGGGCTCCGGGTTCTGGAAAGACGGGGTGA	
103-108	consensus	CtCT-GGAGGGCCTGCCAGGGCCCTGGGCATGGGCTCCGGGTTCTGGAAAGACGGGGTGA	
<u>SEQ ID NO:</u>	<u>ISOLATE</u>		
108	DR4	489 CTATGCAACAGGGAA=tCTTCCTGGTTGCTCTTCTCTATCTTCCCTTTGGCttTGCTCTCT	
103	DK7	489 CTATGCAACAGGGAA=ACTTCCCTGGTTGCTCTTCTCTATCTTCCCTTTGGCCCTGCTCTCT	
104	US11	489 CTATGCAACAGGGAA=ACTTCCCTGGTTGCTCTTCTCTATCTTCCCTTGCTCTCT	
105	S14	489 CTATGCAACAGGGAA=ACTTCCCTGGTTGCTCTTCTCTATCTTCCCTTGCTCTCT	
106	SW1	489 CTATGCAACAGGGAA=ACTTCCCTGGTTGCTCTTCTCTATCTTCCCTTGCTCTCT	
107	S18	489 CTATGCAACAGGGAA=ACTTCCCTGGTTGCTCTTCTCTATCTTCCCTTGCTCTCT	
103-108	consensus	CTATGCAACAGGGAA=ACTTCCCTGGTTGCTCTTCTCTATCTTCCCTTGCTCTCT	

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FIGURE 6A-4

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
108	DR4	550 TGCTTGACCGTGCCGGCaTGGCC
103	DK7	550 TGCCTGACCGTGCCGGCTTGGCC
104	US11	550 TGCCCTGACTGTGCCGGCTTAGCC
105	S14	550 TGCCCTGACTGTGCCGGCTTAGCC
106	SW1	550 TGCCCTGACAGTGCCGGCTAGCC
107	S18	550 TGTCTGACTGTGCCGGCTAGCT
103-108	consensus	TGccCTGACTGTGCCGGCTTCAGCC

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FIGURE 6B-1

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
119	S9	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
117	IND3	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
118	IND8	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
111	D1	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
112	US6	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
113	P10	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
114	DK1	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
115	T10	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
116	SW2	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
122	HK4	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
109	SA10	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
110	S45	1 ATGAGCACCGAATCCTTAACCTCAAAAGACAACCAAAACGTAACACCAACCCGGCCCCACAGG
123	P8	1 ATGAGCACCGACTCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
124	T3	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
120	HK3	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
121	HK5	1 ATGAGCACCGAATCCTTAACCTCAAAAGAAAAACCAAAACGTAACACCAACCCGGCCCCACAGG
109-124	consensus	ATGAGCACCGAatCCTTAACCTCAAAAGAaAaACCAAAACGTAACACCAaCCGGCCCCACAGG

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FIGURE 6B-2

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
119	S9	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
117	IND3	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
118	IND8	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
111	D1	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
112	US6	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
113	P10	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
114	DK1	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
115	T10	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
116	SW2	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
122	HK4	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
109	SA10	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
110	S45	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
123	P8	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
124	T3	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
120	HK3	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
121	HK5	62 ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG
109-124	consensus	ACGTCAAGTCCCCGGGGTGGtCAGATCGTcGGTGAGTTAACCTGTTGGCCAGGGG

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FIGURE 6B-3

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
119	S9	
117	IND3	CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
118	IND8	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
111	D1	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
112	US6	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
113	P10	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
114	DK1	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
115	T10	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
116	SW2	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
122	HK4	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
109	SA10	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
110	S45	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTcaACACCTCGTGGACGG
123	P8	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCAACCTCGTGGCAGG
124	T3	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
120	HK3	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
121	HK5	123 CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGAAAGG
109-124	consensus	CCCCAGGTGGGTGTCGGCGCACTAGGAAGACTTCCGAGCCGGTGGCAACCTCGTGGaaGG

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FIGURE 6B-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
119	S9	
117	IND3	184 CGACAACCTATCCCCAAGGCTGCCatCCCGAGGGCAGGGCCtCGGCTAGCCCCGGTAC
118	IND8	184 CGACAACCTATCCCCAAGGCTCGCCGGCCGGCCGAGGGTAGGGCTAGGGCTAGCCCCGGGACC
111	D1	184 CGACAACCTATCCCCAAGGCTCGCCGGCCGGCCGAGGGTAGGGCTAGGGCTAGCCCCGGGTAC
112	US6	184 CGACAACCTATCCCCAAGGCTCGCCGGCCGGCCGAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
113	P10	184 CGACAACCTATCCCCAAGGCTCGCCGGCCGGCCGAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
114	DK1	184 CGACAACCTATCCCCAAGGCTCGCCGGCCGGCCGAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
115	T10	184 CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
116	SW2	184 CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
122	HR4	184 CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
109	SA10	184 CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
110	S45	184 CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
123	P8	184 CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
124	T3	184 CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
120	HK3	184 CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
121	HK5	184 CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCTAGGGCTAGCCCCGGGTAC
109-124	consensus	CGACAACCTATCCCCAAGGCTCGCCAGGGCAGGGCAGGGCTAGCCCCGGGTAC

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FIGURE 6B-5

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
11.9	S9	CCTGGCCCCCTCTACGGCAATGAGGGCTTGGGTGGCAGGATGGCTCCTGTCACCCCGtGG
11.7	IND3	CCTGGCCCCCTCTATGGCAATGAGGGCTTGGGTGGCAGGATGGCTCCTGTCACCCCGGGG
11.8	IND8	CCTGGCCCCCTCTATGGCAATGAGGGCTTGGGTGGCAGGATGGCTCCTGTCACCCCGGGG
11.1	D1	CCTGGCCCCCTCTATGGCAACGAGGGCTTGGGTGGCAGGATGGCTCCTGTCACCCCGGGG
11.2	US6	CCTGGCCCCCTCTATGGCAACGAGGGCTTGGGTGGCAGGATGGCTCCTGTCACCCCGTGG
11.3	P10	CCTGGCCCCCTCTATGGCAACGAGGGCATGGGTGGCAGGATGGCTCCTGTCACCCCGTGG
11.4	DK1	CCTGGCCCCCTCTATGGCAATGAGGGCTTGGGTGGCAGGATGGCTCCTGTCACCCCGGGG
11.5	T10	CCTGGCCCCCTCTATGGCAATGAGGGCATGGGTGGCAGGATGGCTCCTGTCACCCCGTGG
11.6	SW2	CCTGGCCCCCTCTATGGCAATGAGGGCATGGGTGGCAGGATGGCTCCTGTCACCCCGGGG
12.2	HK4	CCTGGCCCCCTCTATGGCAATGAGGGCATGGGTGGCAGGATGGCTCCTGTCACCCCGGGG
10.9	SA10	CCTGGCCCCCTCTATGGCAATGAGGGCTTGGGTGGCAGGATGGCTCCTGTCACCCCGTGG
11.0	S45	CCTGGCCCCCTCTATGGCAATGAGGGCTTGGGTGGCAGGATGGCTCCTGTCACCCCGTGG
12.3	P8	CCTGGCCCCCTCTATGGCAATGAGGGCTTGGGTGGCAGGATGGCTCCTGTCACCCCGGGG
12.4	T3	CCTGGCCCCCTCTATGGCAACGAGGGCATGGGTGGCAGGATGGCTCCTGTCACCCCGGGG
12.0	HK3	CCTGGCCCCCTCTATGGCAACGAGGGCATGGGTGGCAGGATGGCTCCTGTCACCCCGGGG
12.1	HK5	CCTGGCCCCCTCTATGGCAATGAGGGCATGGGTGGCAGGATGGCTCCTGTCACCCCatGG
109-124	consensus	CttTGGCCCCCTATGgCaAtGAGGGC-TGGGgtGGGGCAGGATGGCTCCTGTCACCCCGcgGG

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FIGURE 6B-6

SEQ_ID NO.:	ISOLATE	
1119	S9	306 CTCTGGCCCTAGTTGGGCCCCAatGACCCCCGGCGTAGGTCGGCTAAATTGGGTAAAGTC
1117	IND3	306 TTCTCGGCCCTAGTTGGGCCCCACAGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1118	IND8	306 CTCTCGGCCCTAGTTGGGCCCCACAGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1111	D1	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1112	US6	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1113	P10	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1114	DK1	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1115	T10	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1116	SW2	306 CTCTCGGCCCTAGTTGGGCCCCACGTGGGCCCCACTGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1122	HK4	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
109	SA10	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1110	S45	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1123	P8	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
124	T3	306 CTCTCGGCCCTAATTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
120	HK3	306 CTCTCGGCCCTAATTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
121	HK5	306 CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC
1109-124	consensus	CTCTCGGCCCTAGTTGGGCCCCACGGACCCCCGGCGTAGGTCGGCTAAATTGGTAAAGTC

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FIGURE 6B-7

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FIGURE 6B-8

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
1119	S9	
1117	IND3	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1118	IND8	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1111	D1	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1112	US6	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1113	P10	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1114	DK1	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1115	T10	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1116	SW2	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1122	HK4	428 CCTTAAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1019	SA10	428 CCTTAAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1110	S45	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1213	P8	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1214	T3	428 CCTTAAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1210	HK3	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
1211	HK5	428 CCCTAGGGGGCGCTGCCAGGGGCTCTGGCCATGGGCTCCGGTtCTGGAGGGACGGCGGTGAA
109-124	consensus	CcctAGGGGGGCGCTGCCAGGGGCTGGGgCATGGGCTCCGGGtCtGGAGGGACGGCGGTGAA

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FIGURE 6B-9

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
119	S9	
117	IND3	489 CTATGCAACAGGGAACTCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
118	IND8	489 CTATGCAACAGGGAACTGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
111	D1	489 tATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
112	US6	489 CTATGCAACAGGGAACTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
113	P10	489 CTATGCAACAGGGAACTGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
114	DK1	489 CTACGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
115	T10	489 CTATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
116	SW2	489 CTATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
122	HK4	489 CTATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
109	SA10	489 CTATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
110	S4.5	489 CTATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
123	P8	489 CTATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
124	T3	489 tATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
120	HK3	489 CTATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
121	HK5	489 CTACGCAACAGGGAAATTACCCGGGAAATTGGCCCGGTTGCTCTTCTATCTTCCTCTTGCTgtTCC
109-124	consensus	cTATGCAACAGGGAAATTGGCCCGGTTGCTCTTCTCTATCTTCCTCTTGCTgtTCC

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FIGURE 6B-10

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
119	S9	550 TGTTTGACCATCCAGCTTCCGGCT
117	IND3	550 TGTTTGACCATCCAGCTTCCGGCT
118	IND8	550 TGTTTGACCGTCCCAGCTTCCGGCT
111	D1	550 TGTTTGACCATCCAGCTTCCGGCT
112	US6	550 TGTTTGACCATCCAGCTTCCGGCT
113	P10	550 TGcctTGACCATCCAGCTTCCGGCT
114	DK1	550 TGTTTGACCATCCAGCTTCCGGCT
115	T10	550 TGTCTTGACCATCCAGCTTCCGGCT
116	SW2	550 TGTCTTGACCATCCAGCTTCCGGCT
122	HK4	550 TGTTTGACCATCCAGCTTCCGGCT
109	SA10	550 TGTTTGACCATCCAGCTTCCGGCT
110	S45	550 TGCTTGACCATCCAGCTTCCGGCT
123	P8	550 TGtCTTGACCATCCAGCTTCCGGCT
124	T3	550 TGCTTGACCATCCAGCTTCCGGCT
120	HK3	550 TGCTTGACCAACCCAGCTTCCGGCT
121	HK5	550 TGtCTTGACCAACCCAGCTTCCGGCT
109-124	consensus	TGttTGACCATCCAGCTTCCGGCT

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FIGURE 6C-1

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
119	S9	
117	IND3	ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
118	IND8	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
111	D1	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
112	US6	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
113	P10	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
114	DK1	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
115	T10	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
116	SW2	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
122	HK4	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
109	SA10	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
110	S45	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
123	P8	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
124	T3	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
120	HK3	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
121	HK5	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGGCCAACAGG
108	DR4	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGTGGCCACAGG
104	US11	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGTGGCCACAGG
105	S14	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGTGGCCACAGG
106	SW1	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGTGGCCACAGG
107	S18	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGTGGCCACAGG
103	DK7	1 ATGAGCACCGAATCCTAAACCTCAAGAAAACCACCAACCGTAACACCAACCGTGGCCACAGG
103-124	consensus	ATGAGCACCGAatCCTAAACCTCAAAGAAaAaACCAAAAGTAACACCAaCCGCGGCCACAGG

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FIGURE 6C-2

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
119	S9	62 ACGTtAA GTTCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
117	IND3	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
118	IND8	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
111	D1	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
112	US6	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
113	P10	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
114	DK1	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
115	T10	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
116	SW2	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
122	HK4	62 ACGTtAA GTTCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
109	SA10	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
110	S45	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
123	P8	62 ACGTtAA GTTCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
124	T3	62 ACGTtAA GTTCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
120	HK3	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
121	HK5	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
108	DR4	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
104	US11	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
105	S14	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
106	SW1	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
107	S18	62 ACGTtAA GTTCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
103	DK7	62 ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG
103-124	consensus	ACGTCAAGT TCCGGGGGTGG CAGATC GT CGGTGAGTTAACCTGTTGCCGGCAAGGGG

**NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6C-3

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
119	S9	123 CCCAGGTTGGGTGTGGCGGaaACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
117	IND3	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
118	IND8	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
111	D1	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
112	US6	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
113	P10	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
114	DK1	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
115	T10	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
116	SW2	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
122	HK4	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
109	SA10	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
110	S45	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGACGG
123	P8	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGACGG
124	T3	123 CCCAGGTTGGGTGTGGCGGACTAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
120	HK3	123 CCCAGGTTGGGTGTGGCGGACCAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
121	HK5	123 CCCAGGTTGGGTGTGGCGGACCAGGAAGACTTCCGAGGGTCGCAACCTCGTGGAAAGG
108	DR4	123 CCCTAGATGGGTGTGGCGGAGGAAAGACTTCCGAGGGTCGCAACCTCGAGGTAGA
104	US11	123 CCCTAGATGGGTGTGGCGGAGGAAAGACTTCCGAGGGTCGCAACCTCGAGGTAGA
105	S14	123 CCCTAGATGGGTGTGGCGGAGGAAAGACTTCCGAGGGTCGCAACCTCGAGGTAGA
106	SW1	123 CCCTAGATGGGTGTGGCGGAGGAAAGACTTCCGAGGGTCGCAACCTCGAGGTAGA
107	S18	123 CCCTAGATGGGTGTGGCGGAGGAAAGACTTCCGAGGGTCGCAACCTCGAGGTAGA
103	DK7	123 CCCTAGATGGGTGTGGCGGAGGAAAGACTTCCGAGGGTCGCAACCTCGAGGTAGA
103-124	consensus	CCCcaGgTGGGTGTGGCGGgactAGGAAGACTTCCGAGGGTCGCAACCTCGtGCaagg

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1...

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FIGURE 6C-4

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6C-5

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
11.9	S9	245 CTTGGCCCCCTCTACGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGtGG
11.7	IND3	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
11.8	IND8	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
11.1	D1	245 CTTGGCCCCCTCATGGCAACGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
11.2	US6	245 CTTGGCCCCCTCATGGCAACGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
11.3	P10	245 CTTGGCCCCCTCATGGCAACGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
11.4	DK1	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
11.5	T10	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
11.6	SW2	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
12.2	HK4	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
10.9	SA10	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
11.0	S45	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
12.3	P8	245 CTTGGCCCCCTCATGGCAACGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
12.4	T3	245 CTTGGCCCCCTCATGGCAACGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
12.0	HK3	245 CTTGGCCCCCTCATGGCAACGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
12.1	HK5	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCATGG
10.8	DR4	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
10.4	US11	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
10.5	S14	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
10.6	SW1	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
10.7	S18	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
10.3	DK7	245 CTTGGCCCCCTCATGGCAATGAGGGCTTGGGTGGGAGGATGGCTCCTGTCACCCCGGG
103-124	consensus	CtTGGCCCCCTCATGGCAAtGAGGGCttGGgtGGGAGGATGGCTCCTGTCACCCCGGtGG

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FIGURE 6C-6

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
119	S9	306 CTCTCGGGCTAGTTGGGGCCCAatGACCCCCGGGTAGGGTGGCTAATTGGGTAAAGTC
117	IND3	306 tTCTCGGGCTAGTTGGGGCCCAAGACCCCCGGTAGGGTGGCTAATTGGGTAAAGTC
118	IND8	306 CTCTCGGGCTAGTTGGGGCCCAAGACCCCCGGTAGGGTGGCTAATTGGGTAAAGTC
111	D1	306 CTCTCGGGCTAGTTGGGGCCCAAGACCCCCGGTAGGGTGGCTAATTGGGTAAAGTC
112	US6	306 CTCTCGGGCTAGTTGGGGCCCAAGACCCCCGGTAGGGTGGCTAATTGGGTAAAGTC
113	P10	306 CTCTCGGGCTAGTTGGGGCCCAAGACCCCCGGTAGGGTGGCTAATTGGGTAAAGTC
114	DK1	306 CTCTCGGGCTAGTTGGGGCCCAAGACCCCCGGTAGGGTGGCTAATTGGGTAAAGTC
115	T10	306 CTCTCGGGCTAGTTGGGGCCCAAGACCCCCGGTAGGGTGGCTAATTGGGTAAAGTC
116	SW2	306 CTCTCGGGCTAGTTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
122	HK4	306 CTCTCGGGCTAGTTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
109	SA10	306 CTCTCGGGCTAGTTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
110	S45	306 CTCTCGGGCTAGTTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
123	P8	306 CTCTCGGGCTAGTTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
124	T3	306 CTCTCGGGCTAATTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
120	HK3	306 CTCTCGGGCTAATTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
121	HK5	306 CTCTCGGGCTAATTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
108	DR4	306 CTCTCGGGCTAATTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
104	US11	306 CTCTCGGGCTAATTGGGGCCCACTGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
105	S14	306 CTCTCGGGCTAGCTGGGGCCCAAGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
106	SW1	306 CTCTCGGGCTAGCTGGGGCCCTACAGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
107	S18	306 CTCTCGGGCTAGCTGGGGCCCTACAGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
103	DK7	306 CTCTCGGGCTAGCTGGGGCCCAAGACCCCCGGCTAGGTGGCTAATTGGGTAAAGTC
103-124	consensus	

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FIGURE 6C-7

SEQ ID NO:	ISOLATE	
119	S9	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTGGCTCGGGGCC
117	IND3	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATCCGGTCTGGGGCC
118	IND8	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATCCGGTCTGGGGCC
111	D1	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATCCGGTCTGGGGCC
112	US6	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATCCGGTCTGGGGCC
113	P10	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATCCGGTCTGGGGCC
114	DK1	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATCCGGTCTGGGGCC
115	T10	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
116	SW2	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
122	HK4	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
109	SA10	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
110	S45	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
123	P8	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
124	T3	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
120	HK3	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
121	HK5	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
108	DR4	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
104	US11	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
105	S14	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
106	SW1	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
107	S18	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
103	DK7	367 ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC
103-124	consensus	ATCGATAACCTCACATGGGCTTtGCCGACCTCATGGGGTACATTCCGGTCTGGGGCC

FIGURE 6C-8

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
119	S9	
117	IND3	428 CCCTAGGGGGGCTGCCAGGGCATGGGCTCCGGGTCTGGGCAATGGGCTCGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
118	IND8	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
111	D1	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
112	US6	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
113	P10	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
114	DK1	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
115	T10	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
116	SW2	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
122	HK4	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
109	S10	428 CTTTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
110	S45	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
123	P8	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
124	T3	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
120	HK3	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAACGGTCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
121	HK5	428 CCCTAGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAACGGTCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
108	DR4	428 CCCTGGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAACGGTCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
104	US11	428 CTCCTGGGAGGGCTGCCAGGGCCTGGGCATGGGCTGGGCAACGGTCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
105	S14	428 CcCTGGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAACGGTCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
106	SW1	428 CTCTGGAGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAACGGTCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
107	S18	428 CTCTGGAGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAACGGTCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
103	DK7	428 CTCTGGAGGGGTGGCTGCCAGGGCCTGGGCATGGGCTGGGCAACGGTCTGGGCAATGGGCTCGGGGTCTGGGAGCGGGGTGAA
103-124	consensus	CccTaGGGGGGGTGGCTGCCAGGGCCTGGGCATGGGCTCGGGGTCTGGGAGCGGGGTGAA

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FIGURE 6C-9

SEQ ID NO:	ISOLATE	SEQUENCE
1119	S9	CTATGCAAACAGGGAAACCTCCCCGGTTGGCTTTCCTATCTCCCTTCTggGCTTTGGCTgtGCC
1117	IND3	CTATGCAAACAGGGAAACCTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTATGCC
1118	IND8	CTATGCAAACAGGGAAACCTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTATGCC
1111	D1	CTATGCAAACAGGGAAATTTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
1112	US6	CTATGCAAACAGGGAAACTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
1113	P10	CTATGCAAACAGGGAAATCTGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
1114	DK1	CTATGCAAACAGGGAAATTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
1115	T10	CTATGCAAACAGGGAAATTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
1116	SW2	CTATGCAAACAGGGAAATCTGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
1222	HK4	CTATGCAAACAGGGAAATTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
109	SA10	CTATGCAAACAGGGAAATTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
1110	S45	CTATGCAAACAGGGAAATTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
123	P8	CTATGCAAACAGGGAAATCTGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
124	T3	CTATGCAAACAGGGAAATTGGCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
120	HK3	CTATGCAAACAGGGAAATTACCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
121	HK5	CTATGCAAACAGGGAAATAACCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
108	DR4	CTATGCAAACAGGGAAATCTCCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
104	US11	CTATGCAAACAGGGAAACCTTCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
105	S14	CTATGCAAACAGGGAAACCTTCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
106	SW1	CTATGCAAACAGGGAAACCTTCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
107	S18	CTATGCAAACAGGGAAACCTTCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
103	DK7	CTATGCAAACAGGGAAACCTTCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC
103-124	consensus	CTATGCAAACAGGGAAACCTTCCGGTTGGCTTTCCTATCTCCCTTCTggCTTTGGCTGTGCC

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FIGURE 6C-10

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
119	S9	TGTTTGACCATCCAGCTTCCGGCT
117	IND3	550 TGTTTGACCATCCAGCTTCCGGCT
118	IND8	550 TGTTTGACCGTCCCAGCTTCCGGCT
111	D1	550 TGTTTGACCATCCAGCTTCCGGCT
112	US6	550 TGTTTGACCATCCAGCTTCCGGCT
113	P10	550 TGccTGACCATCCAGCTTCCGGCT
114	DK1	550 TGTTTGACCATCCAGCTTCCGGCT
115	T10	550 TGTTTGACCATCCAGCTTCCGGCT
116	SW2	550 TGTCTTGACCATCCAGCTTCCGGCT
122	HK4	550 TGTTTGACCATCCAGCTTCCGGCT
109	SAL0	550 TGTTTGACCATCCAGCTTCCGGCT
110	S45	550 TGCTTGACCATCCAGCTTCCGGCT
123	P8	550 TGtctTGACCATCCAGCTTCCGGCT
124	T3	550 TGCTTGACCATCCAGCTTCCGGCT
120	HK3	550 TGCTTGACCACCCCAGCTTCCGGCT
121	HK5	550 TGtctTGACCACCCCAGCTTCCGGCT
108	DR4	550 TGCTTGACCGTGCCGGCatTCGGCC
104	US11	550 TGCCCTGACTGTGCCGGCTTCAGCC
105	S14	550 TGCCTTGACTGTGCCGGCTTCAGCC
106	SW1	550 TGCCTTGACAGTGGCCGGTCAAGCC
107	S18	550 TGtCTTGACTGTGCCGGTCAAGCT
103	DK7	550 TGCCTTGACCGTGCCGGCTTCAGCC
103-124	consensus	TGttTgAccatcCCaGctTCCGGCT

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FIGURE 6D-1

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>		
128	T2	1 ATGAGCACAAATCCTAACCTCAAGAAAACCCAAAGAACACTAACCGTGTGCCACAAAG	
125	T4	1 ATGAGCACAAATCCTAACCTCAAGAAAACCCAAAGAACACCCACCGTGTGCCACAGG	
126	US10	1 ATGAGCACAAATCCTAACCTCAAGAAAACCCAAAGAACACCAACCGTGTGCCACAAAG	
127	T9	1 ATGAGCACAAATCCTAACCTCAAGAAAACCCAAAGAACACCCACCGTGTGCCACAGG	
125-128	consensus	ATGAGCACAAATCCTAACCTCAAAGAAAACCCAAAGAACACCAACCGTGTGCCACACA-G	
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>		
128	T2	62 ACGTTAAGTTCCGGGGGGCCAGATCGTTGGGGAGTTACCTTGTGCCGGCAGGGG	
125	T4	62 ACGTTAAGTTCCGGGGGGCCAGATCGTTGGGGAGTTACCTTGTGCCGGCAGGGG	
126	US10	62 ACGTTAAGTTCCGGGGGGCCAGATCGTTGGGGAGTTACCTTGTGCCGGCAGGGG	
127	T9	62 ACGTTAAGTTCCGGGGGGCCAGATCGTTGGGGAGTTACCTTGTGCCGGCAGGGG	
125-128	consensus	ACGTTAAGTTCCGGGGGGCCAGATCGTTGGGGAGTTACCTTGTGCCGGCAGGGG	
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>		
128	T2	123 CCCCAGGTTGGGTGTGGGGGACAAGGAAGACTTCGGAGGGTCCCAAGCTCGTGGaaAGG	
125	T4	123 CCCCAGGTTGGGTGTGGGGGACAAGGAAGACTTCGGAGGGATCCAGGCCAGTGGGGAGG	
126	US10	123 CCCCAGGTTGGGTGTGGGGGACAAGGAAGACTTCGGAGGGTCCCAAGCTCGTGGaaAGG	
127	T9	123 CCCtAGGTTGGGTGTGGGCaCGACAAGGAAGACTTCGGAGGGTCCCAAGCTCGTGGaaAGG	
125-128	consensus	CCCCAGGTTGGGTGTGGGGACAAGGAAGACTTCGGAGGGTCCCAAGCTCGTGGaaAGG	
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>		
128	T2	184 CGCCAGCCCATCCCCtAAAGATCGGGGTCCACTGGCAAGTCTGGGGAAAACCGGATAAC	
125	T4	184 CGCCAGCCCATCCCCAAAGATCGGGGTCCACTGGCAAGTCTGGGGAAAACCGGATAAC	
126	US10	184 CGCCAGCCCATCCCCAAAGATCGGGGTCCACTGGCAAGTCTGGGGAAAACCGGATAAC	
127	T9	184 CGCCAGCCCATCCCCAAAGATCGGGGTCCACTGGCAAGTCTGGGGAAAACCGGATAAC	
125-128	consensus	CGCCAGCCCATCCCCAAAGATCGGGGTCCACTGGCAAGTCTGGGGAAAACCGGATAAC	

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FIGURE 6D-2

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	245 CCTGGCCCCCTGTATGGAAATGAGGGCTGGGCAAGGATGGCTCTGTCCCCCGAGG
125	T4	245 CCTGGCCCCCTGTATGGAAATGAGGGACTGGCTGGGAGATGGCTCTGTCCCCCGAGG
126	US10	245 CTGGCCCCATATGGAAATGAGGGACTGGCTGGGAGATGGCTCTGTCCCCCGAGG
127	T9	245 CCTGGCCCCATATGGAAATGAGGGACTGGCTGGGAGATGGCTCTGTCCCCCGAGG
125-128	consensus	CCTGGCCCC-TATGGAAATGAGGGACTCGGCTGGGAGATGGCTCTGTCCCCCGAGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	306 TTCTCGTCCCTCTTGGGCCCCAATGACCCCCGGCATAGGTGGCCAATGTTGGTAAAGTC
125	T4	306 TTCCCGTCCCTCTTGGGCCCCAATGACCCCCGGCATAGGTGGCCAACGTTGGTAAGGTC
126	US10	306 TTCCCGTCCCTCTTGGGCCCCACTGATCCCCGGCATAGGTGGCCAACGTTGGTAAGGTC
127	T9	306 TTCCCGTCCCTCTTGGGCCCCAGTGACCCCCGGCATAGGTGGCCAACGTTGGTAAGGTC
125-128	consensus	TTCCCGTCCCTCTTGGGCCCCAATGACCCCCGGCATAGGTGGCCAACGTTGGTAAGGTC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	367 ATCGATAACCTTAACGTGGCCTTGCCGACCTCATGGGTACATCCCCGTCTAGGGGCC
125	T4	367 ATCGATAACCTTAACGTGGCCTTGCCGACCTCATGGGTACGTTCCCCGTCTAGGGGCC
126	US10	367 ATCGATAACCTTAACGTGGCCTTGCCGACCTCATGGGTACATCCCCGTCTAGGGGCC
127	T9	367 ATCGATAACCTTAACGTGGCCTTGCCGACCTCATGGGTACATCCCCGTCTAGGGGCC
125-128	consensus	ATCGATAACCTTAACGTGGCCTTGCCGACCTCATGGGTACATCCCCGTCTAGGGGCC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	428 CGCTGGTGGGTGAGAGTCTGGGAGTGGCTCTGGAGACTGGTAA
125	T4	428 CGTTGGTGGGTGAGAGTCTGGGAGTGGCTCTGGAGACTGGTAA
126	US10	428 CGCTGGTGGGTGAGAGTCTGGGAGTGGCTCTGGAGACTGGTAA
127	T9	428 CGCTGGTGGGTGAGAGTCTGGGAGTGGCTCTGGAGACTGGTAA
125-128	consensus	CGCTGGTGGGTGAGAGTCTGGGAGTGGCTCTGGAGACTGGTAA

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FIGURE 6D-3

<u>SEQ ID NO:</u>	<u>ISOLATE</u>		
128	T2	489	TTATGCAACAGGtAACTTACCCGGTTGCTCCTTCTATcTTTGCTTATcTTTGCTGCCCTgCTGTCC
125	T4	489	TTATGCAACAGGGAACtTACCTGGTGGCTCCTTCTATTTCTATTTCTATTTCTATCTTCTTGCTGCCCTACTGTCC
126	US10	489	TTATGCAACAGGGAACtTACCCGGTTGCTCCTTCTATTTCTATCTTCTTGCTGCCCTACTGTCC
127	T9	489	TTATGCAACAGGGAACtTACCTGGTGGCTTCTTTCTATCTTCTTGCTGCCCTACTGTCC
125-128	consensus		TTATGCAACAGGgAACTTACCC-GGTTGCTCCttttCTATcTTTGCTGCCCTACTGTCC

<u>SEQ ID NO:</u>	<u>ISOLATE</u>		
128	T2	550	TGCATCACtATTCCGGTtTCAGCT
125	T4	550	TGCATCACCATTCGAGTCTCCGCT
126	US10	550	TGCATCACCATTCGAGTCTCTGCT
127	T9	550	TGCATCACCACTCCGGCTCTGCT
125-128	consensus		TGCATCACCAATTCC-GtctCTtGCT

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FIGURE 6E-1

<u>SEQ_ID</u>	<u>ID_NO.</u>	<u>ISOLATE</u>	<u>SEQ_ID</u>	<u>ID_NO.</u>	<u>ISOLATE</u>	<u>SEQ_ID</u>	<u>ID_NO.</u>	<u>ISOLATE</u>
131	DK11	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAATACAAACGCCACAGG	131	DK11	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAATACAAACGCCACAGG	129	T8	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAACAAACGCCACAGG
132	SW3	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAATACAAACGCCACAGG	132	SW3	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAATACAAACGCCACAGG	130	US1	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAACAAACGCCACAGG
133	DK8	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAATACAAACGCCACAGG	133	DK8	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAATACAAACGCCACAGG	129	T8	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAACAAACGCCACAGG
129	T8	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAACAAACGCCACAGG	129	T8	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAACAAACGCCACAGG	130	US1	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAACAAACGCCACAGG
129-133	consensus	ATGAGCACAAATCCTAACCTCAAGAAAAACCAAAAGAAACACAACAAACGCCACAGG	129-133	consensus	ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	129-133	consensus	ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG
131	DK11	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	131	DK11	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	130	US1	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG
132	SW3	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	132	SW3	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	130	US1	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG
133	DK8	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	133	DK8	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	129	T8	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG
129	T8	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	129	T8	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	130	US1	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG
130	US1	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	130	US1	62 ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG	129-133	consensus	ACGTTAAGTTCCGGTGGCCAGATCGTTGGGGAGTTACTTGCTGGCCAGGG
129-133	consensus	CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	129-133	consensus	CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	130	US1	CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG
131	DK11	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	131	DK11	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	132	SW3	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG
132	SW3	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	132	SW3	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	133	DK8	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG
133	DK8	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	133	DK8	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	129	T8	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG
129	T8	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	129	T8	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	130	US1	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG
130	US1	123 CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	129-133	consensus	CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG	129-133	consensus	CCCCAGCTTGGGTGGCCAGACAAGGAAGACTTCCGAGGGATCCAGCCGGCTGGAG

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FIGURE 6E-2

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
131	DK11	184 CGCCAGCCCATCCGAAAGATCGGGCTCACCGGAAGCCTGGAAAGCCAGGATATC
132	SW3	184 CGCCAGCCCATCCGAAAGATCGGGCTCACCGGAAGCCTGGAAAGCCAGGATATC
133	DK8	184 CGCCAGCCCATCCGAAAGATCGGGCTCACCGGAAGCCTGGAAAGCCAGGATATC
129	T8	184 CGCCAGCCCATCCGAAAGATCGGGCTCACCGGAAGCCTGGAAAGCCAGGATATC
130	US1	184 CGCCAGCCCATCCGAAAGATCGGGCTCACCGGAAGCCTGGAAAGCCAGGATATC
129-133	consensus	CGCCAGCCCATCCGAAAGATCGGGCTCACCGGAAGCCTGGAAAGCCAGGATATC
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
131	DK11	245 CTGGCCCCCTGTATGGAAACGAGGGCTGGGGCTGGGCAGGTTGGCTCCTGTCCTGGGG
132	SW3	245 CTGGCCCCCTGTATGGAAACGAGGGCTGGGGCTGGGCAGGTTGGCTCCTGTCCTGGGG
133	DK8	245 CTGGCCCCCTGTATGGAAACGAGGGCTGGGGCTGGGCAGGTTGGCTCCTGTCCTGGGG
129	T8	245 CTGGCCCCCTGTATGGAAACGAGGGCTGGGGCTGGGCAGGTTGGCTCCTGTCCTGGGG
130	US1	245 CTGGCCCCCTGTATGGAAACGAGGGCTGGGGCTGGGCAGGTTGGCTCCTGTCCTGGGG
129-133	consensus	CTGGCCCCCTGTATGGAAACGAGGGCTGGGGCTGGGCAGGTTGGCTCCTGTCCTGGGG
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
131	DK11	306 GTCTCATCCTAATTGGGGCCCACTGACCCCCGGCATATAATCAGCAATTGGGTAAGTC
132	SW3	306 GTCTCATCCTAATTGGGGCCCACTGACCCCCGGCATAGATCAGCAATTGGGCAAGTC
133	DK8	306 GTCTCGTCCCTACTGGGGCCCACTGACCCCCGGCATAGATCAGCAATTGGGCAAGTC
129	T8	306 GTCTCGTCCCTACTGGGGCCCACTGACCCCCGGCATAGATCAGTAATTGGGCAAGAGTC
130	US1	306 GTCTCGTCCCTACTGGGGCCCACTGACCCCCGGCATAGATCAGTAATTGGGCAAGGTC
129-133	consensus	GTCCTGTCCTACTGGGGCCCACTGACCCCCGGCATAGATCAGCAATTGGGCAAGGTC

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FIGURE 6E-3

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
131	DK11	367 ATCGACACCAATTACGGTGTGGTTGCCGACCTCATGGGTACATCCCTGTCGTCGGGCC
132	SW3	367 ATCGACACCAATTACGGTGTGGTTGCCGACCTCATGGGTACATCCCTGTCGTCGGGCC
133	DK8	367 ATCGACACCAATTACGGTGTGGTTGCCGACCTCATGGGTACATCCCTGTCGTCGGGCC
129	T8	367 ATCGATAACCAATTACGGTGTGGTTGCCGACCTCATGGGTACATCCCTGTCGTCGGGCC
130	US1	367 ATCGATAACCAATTACGGTGTGGTTGCCGACCTCATGGGTACATCCCTGTCGTCGGGCC
129-133	consensus	ATCGACACCAATTACGGTGTGGTTGCCGACCTCATGGGTACATCCCTGTCGTCGGGCC
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
131	DK11	428 CGGTGGAGGGCGTCCGAGGGTCTGGCACACGGTCTGGTAGAGTCCTGGAAAGACGGATAAA
132	SW3	428 CGGTGGAGGGCGTCCGAGGGTCTGGCACACGGTCTGGTAGAGTCCTGGAAAGACGGATAAA
133	DK8	428 CGGTGGAGGGCGTCCGAGGGTCTGGCACACGGTCTGGTAGAGTCCTGGAAAGACGGATAAA
129	T8	428 CGGTGGAGGGCGTCCGAGGGTCTGGCACACGGTCTGGTAGAGTCCTGGAAAGACGGATAAA
130	US1	428 CGGTGGAGGGCGTCCGAGGGTCTGGCACACGGTCTGGTAGAGTCCTGGAAAGACGGATAAA
129-133	consensus	CGGTGGAGGGCGTCCGAGGGTCTGGCACACGGTCTGGTAGAGTCCTGGAAAGACGGATAAA
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
131	DK11	489 TTACGGCAACACGGGAATTCTGCCTGGTTGGCTCTTCTATCTTCTACTTGCTCTTGTGCa
132	SW3	489 TTACGGCAACACGGGAATTCTGCCTGGTTGGCTCTTCTATCTTCTACTTGCTCTTGTGCG
133	DK8	489 TTACGGCAACACGGGAATTCTGCCTGGTTGGCTCTTCTATCTTCTACTTGCTCTTGTGCG
129	T8	489 CTATGCAACACGGGAATTCTGCCTGGTTGGCTCTTCTATCTTCTACTTGCTCTTGTGCG
130	US1	489 TTACGGCAACACGGGAATTCTGCCTGGTTGGCTCTTCTATCTTCTACTTGCTCTTGTGCG
129-133	consensus	ttACGGCAACACGGGAATTCTGCCTGGTTGGCTCTTCTATCTTCTACTTGCTCTTGTGCG

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FIGURE 6E-4

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
131	DK11	550 TGCTgCACAGTGCCAGTGTCTGCG
132	SW3	550 TGCTtCACAGTGCCAGTGTCTGCG
133	DK8	550 TGCTgCACAGTGCCAGTGTCTGCG
129	T8	550 TGCTtCACAGTGCCAGTGTCTGCA
130	US1	550 TGGgcCACgGTGCCgGTGTCTGCA
129-133	consensus	TGCT - CACAGTGCCAGTGTCTGCG

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FIGURE 6F-1

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>		<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
131	DK11		131	DK11	
132	SW3		132	ACGTTAAGTCCCCGGGTGGCGCCAGATCGTTGGCAGTTACTTGTGCGGCCACAGGG	62
133	DK8		132	ACGTTAAGTCCCCGGGTGGCGCCAGATCGTTGGCAGTTACTTGTGCGGCCACAGGG	62
129	T8C		133	ACGTTAAGTCCCCGGGTGGCGCCAGATCGTTGGCAGTTACTTGTGCGGCCACAGGG	62
130	US1		129	ACGTTAAGTCCCCGGGTGGCGCCAGATCGTTGGCAGTTACTTGTGCGGCCACAGGG	62
125	T4		130	ACGTTAAGTCCCCGGGTGGCGCCAGATCGTTGGCAGTTACTTGTGCGGCCACAGGG	62
126	US10		125	ACGTTAAGTCCCCGGGTGGCGCCAGATCGTTGGCAGTTACTTGTGCGGCCACAGGG	62
127	T9		126	ACGTTAAGTCCCCGGGTGGCGCCAGATCGTTGGCAGTTACTTGTGCGGCCACAGGG	62
128	T2		127	ACGTTAAGTCCCCGGGTGGCGCCAGATCGTTGGCAGTTACTTGTGCGGCCACAGGG	62
134	S83		128	ACGTTAAGTCCCCGGGTGGCGCCAGATCGTTGGCAGTTACTTGTGCGGCCACAGGG	62
125-134	consensus		125-134	consensus	
				ACGTTAAGTCCCCGGG-GGCGGGCCAGATCGTTGGCGAGT-TACTTGTGCGGCCACAGGG	

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FIGURE 6F-2

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FIGURE 6F-3

<u>SEQ ID NO:</u>	<u>ISOLATE</u>		
131	DK11		
132	SW3	245 CTTGGCCCCCTGTATGGAAACGAGGGCTGGGCTGGCAGGTGGCTCCCTGTCCCCCGGG	
133	DK8	245 CTTGGCCCCCTGTATGGAAACGAGGGCTGGGCTGGCAGGTGGCTCCCTGTCCCCCGGG	
129	T8	245 CTTGGCCCCCTGTATGGAAACGAGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG	
130	US1	245 CTTGGCCCCCTGTATGGAAACGAGGGCTGGGCTGGGCTGGGCTGGGCTGGG	
125	T4	245 CTTGGCCCCCTGTATGGAAACGAGGGCTGGGACTGGGACTGGGACTGGGACTGGG	
126	US10	245 CTTGGCCCCCTGTATGGAAATGGGAAATGGGAAATGGGAAATGGGAAATGGGAAATGGG	
127	T9	245 CTTGGCCCCCTGTATGGAAATGGGAAATGGGAAATGGGAAATGGGAAATGGGAAATGGG	
128	T2	245 CTTGGCCCCCTGTATGGAAATGGGAAATGGGAAATGGGAAATGGGAAATGGGAAATGGG	
134	S83	245 CTTGGCCCCCTGTATGGAAATGGGAAATGGGAAATGGGAAATGGGAAATGGGAAATGGG	
125-134	consensus	CtTGGCCCCCTGTATGG-AA-GGGG-- CGGCTGGGCAAGGTGGCTCCCTGTCCCCCGGG	
<u>SEQ ID NO:</u>	<u>ISOLATE</u>		
131	DK11	306 GTCTCATCCTAAATTGGGGCCCCACTGACCCCCGGATAAATCACGCAATTGGGTAAGTC	
132	SW3	306 GTCTCATCCTAAATTGGGGCCCCACTGACCCCCGGCAATAGATCACGCAATTGGCAAGTC	
133	DK8	306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCAATAGATCACGCAATTGGCAAGTC	
129	T8	306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCAATAGATCACGTAATTGGCAAGTC	
130	US1	306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCAACAGATCACGTAACCTGGCAAGTC	
125	T4	306 TTCCCGTCCCTCCATTGGGGCCCCATAGGTCGGCAACGTGGTAAGGTC	
126	US10	306 TTCCCGTCCCTCTGGGGCCCCACTGATCCCCGGCATAGGTCGGCAACGTGGTAAGGTC	
127	T9	306 TTCCCGTCCCTCTGGGGCCCCAGTGACCCCCGGCATAGGTCGGCAACGTGGTAAGGTC	
128	T2	306 TTCTCGTCCTCTGGGGCCCCATAGGTCGGCAACGTGGTAAGGTC	
134	S83	306 TTCTCGTCCTCTGGGGCCCCACCGACCCCCGGATAaatCGGCAActTGGTAAGGTC	
125-134	consensus	-TctCgtCCT-ctTGGGGCCCCActGACCCCCGGCAatAgatC-CGCAA-TGGGta-GTC	

**NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6F-4

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6F-5

<u>SEQ_ID</u>	<u>ID NO:</u>	<u>ISOLATE</u>	<u>550</u>	<u>TGCTGCACAGTGCCAGTGTCTGGC</u>
131	DK11		550	TGCTGCACAGTGCCAGTGTCTGGC
132	SW3		550	TGCTGCACAGTGCCAGTGTCTGGC
133	DK8		550	TGCTGCACAGTGCCAGTGTCTGGC
129	T8		550	TGCTGCACAGTGCCAGTGTCTGCA
130	US1		550	TGGGCCACGTGCCGGTGTCTGCA
125	T4		550	TGCATACCATTCCAGTCTCCGCT
126	US10		550	TGCATACCATTCCAGTCTCTGCT
127	T9		550	TGCATACCATTCCGGTTCTGCT
128	T2		550	TGCATCACTATTCCGGTTCAgCT
134	S83		550	TGCATCTCTgtggccaaGTTCCGCC
125-134		<u>consensus</u>		TGGCatCaCaaqtqCCCaAgttgtCTGCT

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FIGURE 6G-1

<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>	<u>DK12</u>	<u>HK10</u>	<u>S52</u>	<u>S2</u>	<u>135-138</u>	<u>consensus</u>	<u>ATGAGCACACTCCCTAAACCTCAAAAGAAAAACCAATTCCGTGCCAACAGG</u>
138			1	1	1	1			ATGAGCACACTCCCTAAACCTCAAAAGAAAAACCAATTCCGTGCCAACAGG
135									ATGAGCACACTCCCTAAACCTCAAAAGAAAAACCAATTCCGTGCCAACAGG
136									ATGAGCACACTCCCTAAACCTCAAAAGAAAAACCAATTCCGTGCCAACAGG
137									ATGAGCACACTCCCTAAACCTCAAAAGAAAAACCAATTCCGTGCCAACAGG
<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>	<u>DK12</u>	<u>HK10</u>	<u>S52</u>	<u>S2</u>	<u>135-138</u>	<u>consensus</u>	<u>ATGAGCACACTCCCTAAACCTCAAAAGAAAAACCAATTCCGTGCCAACAGG</u>
138			62	62	62	62			ACGTcaAGTTCCCGGTGGCGCACAGATCGTGGAGTATACTGTGTGCCGCAGGGG
135				62	62	62			ACGTTAAGTCCCCGGTGGCGCACAGATCGTGGAGTATACTGTGTGCCGCAGGGG
136					62	62			ACGTTAAGTCCCCGGTGGCGCACAGATCGTGGAGTATACTGTGTGCCGCAGGGG
137						62			AcATCAAGTCCCCGGTGGCGCACAGATCGTGGAGTATACTGTGTGCCGCAGGGG
<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>	<u>DK12</u>	<u>HK10</u>	<u>S52</u>	<u>S2</u>	<u>135-138</u>	<u>consensus</u>	<u>ACGT-AAGTTCCCCGGTGGCGCACAGATCGTGGAGTATACTGTGTGCCGCAGGGG</u>
138			123	123	123	123			CCCACGATTGGGTGTGGCGCACGGTAAAACCTCTGAACGGTCacAGCCTGGGACGG
135				123	123	123			CCCACGATTGGGTGTGGCGCACGGTAAAACCTCTGAACGGTCAGCCTGGGACGG
136					123	123			CCCACGATTGGGTGTGGCGCACGGTAAAACCTCTGAACGGTCAGCCTGGGACGG
137						123			CCCACGATTGGGTGTGGCGCACGGTAAAACCTCTGAACGGTCAGCCTGGGACGG
<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>	<u>DK12</u>	<u>HK10</u>	<u>S52</u>	<u>S2</u>	<u>135-138</u>	<u>consensus</u>	<u>CCCACGATTGGGTGTGGCGCACGGTAAAACCTCTGAACGGTCAGCCTGGGACGG</u>
138			184	184	184	184			CGACAGCCTATCCCCAAGGGCGCTGGGAAAGCCGGTCTGGGTCTAGCCTGGGTACCG
135				184	184	184			CGACAGCCTATCCCCAAGGGCGCTGGGAAAGCCGGTCTGGGTCTAGCCTGGGTACCG
136					184	184			CGACAGCCTATCCCCAAGGGCGCTGGGAAAGCCGGTCTGGGTCTAGCCTGGGTACCG
137						184			CGACAGCCTATCCCCAAGGGCGCTGGGAAAGCCGGTCTGGGTCTAGCCTGGGTACCG
<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>	<u>DK12</u>	<u>HK10</u>	<u>S52</u>	<u>S2</u>	<u>135-138</u>	<u>consensus</u>	<u>CGACAGCCTATCCCCAAGGGCGCTGGGAAAGCCGGTCTGGGTCTAGCCTGGGTACCG</u>

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FIGURE 6G-2

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
138	DK12	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGGGAGGTGGCTCCCTGTCGCCACGGGG
135	HK10	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGGGAGGTGGCTCCCTGTCGCCACGGGG
136	S52	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGGGAGGTGGCTCCCTGTCGCCACGGGG
137	S2	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGGGAGGTGGCTCCCTGTCGCCACGGGG
135-138	consensus	CTTGGCCCCCTCTATGGTAACGAGGGCTGGGAGGTGGCTCCCTGTCGCCACGGGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
138	DK12	306 CTCCCGTCCCATCTTGGGGCCAAACGACCCCCGGGagGTCCCGCAATTGGCTAAGTC
135	HK10	306 CTCCCGTCCCATCTTGGGGCCAAACGACCCCCGGGagGTCCCGCAATTGGCTAAGTC
136	S52	306 CTCCCGTCCCATCTTGGGGCCAAACGACCCCCGGGagGTCCCGCAATTGGCTAAGTC
137	S2	306 CTCCCGTCCCATCTTGGGGCCAAATGACCCCCGGGAGGTCCCGCAATTGGCTAAGTC
135-138	consensus	CTCCCGTCCCATCTTGGGGCCAAACGACCCCCGGGagGTCCCGCAATTGGCTAAGTC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
138	DK12	367 ATCGATAACCCTCACGTGGGATTGCCGACTCATGGGTACATCCGCTGTCGGGCTC
135	HK10	367 ATCGATAACCCTCACGTGGGATTGCCGACTCATGGGTACATCCGCTGTCGGGCTC
136	S52	367 ATCGATAACCCTCACGTGGGATTGCCGACTCATGGGTACATCCGCTGTCGGGCTC
137	S2	367 ATCGATAACCCTCACGTGGGATTGCCGACTCATGGGTACATCCGCTGTCGGGCTC
135-138	consensus	ATCGATAACCCTCACGTGGGATTGCCGACTCATGGGTACATCCGCTGTCGGGCTC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
138	DK12	CtGTAGGGGGGTGCGCAAGAGCCCCTCGCGATGGCGTGAAGACGGGATAAA
135	HK10	428 CCGTAGGGGGGTGCGCAAGAGCCCCTCGCGATGGCGTGAAGACGGGATAAA
136	S52	428 CCGTAGGGGGGTGCGCAAGAGCCCCTCGCGATGGCGTGAAGACGGGATAAA
137	S2	428 CCGTAGGGGGGTGCGCAAGAGCCCCTCGCGATGGCGTGAAGACGGGATAAA
135-138	consensus	CcGTAGGaGGGTGCGAAGAGCCCCTCGCGATGGCGTGAAGACGGGATAAA

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FIGURE 6G-3

<u>SEQ_ID NO.:</u>	<u>ISOLATE</u>	
138	DK12	489
135	HK10	489
136	S52	489
137	S2	489
135-138	consensus	TTT-GCAACAGGAACTTGGCCGGTTGCTCCTTTCTATCTTCCTTCTATCTGCTCTGTTCTCT

<u>SEQ_ID NO.:</u>	<u>ISOLATE</u>	
138	DK12	550
135	HK10	550
136	S52	550
137	S2	550
135-138	consensus	TGCTTAATTCAATCCAGGCTAGT

**NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6H-1

**NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...**

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FIGURE 6H-2

<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>	<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>
145	DK13	CGCCAGCCTATCCCCAAGGCGCGCcAAActCGAGGGTAGGTCTGGGCTCAGGCCGGTAC	145	184	CGCCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC
143	Z6	CGCCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC	184	184	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC
144	Z7	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC	184	184	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC
140	Z8	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC	184	184	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC
139	Z4	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC	184	184	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC
142	Z5	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC	184	184	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC
141	Z1	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC	184	184	CGTCAGCCTATCCCCAAGGCAACGTCATCTGAGGAAGGTCTGGGCTCAGGCCGGTAC
139-145	consensus	CGtCAgCCTATCCCCAAGGCAACGtCggtccGAGGGAGgtCTGGGtCAGCCCCGGTAC	145	245	CtTGCCCCCTTA CGGC AATGAGGGCTGGGGTGGGGATGGCTCCTGTCACCCGGGG
			143	245	CATGGCCTCTTACGGTAATGAGGTTAGGGTCTGGGGTGGGGATGGCTCCTGTCACCCGGGG
			144	245	CATGGCCTCTTACGGTAACGAGGTTGGGGTGGGGATGGCTCCTGTCACCCGGGG
			140	245	CATGGCCTCTTACGGTAATGAGGTTGGGGTGGGGATGGCTCCTGTCACCCGGGG
			139	245	CttGGCCCTCATGGCAATGAGGCTGTGGGCAAGGGTGGGGATGGCTCCTGTCACCCGGGG
			142	245	CttGGCCTCTTATGGCAATGAGGCTGTGGGCAAGGGTGGGGATGGCTCCTGTCACCCGGGG
			141	245	CttGGCCCTTACGGCAATGAGGCTGTGGGCAAGGGTGGGGATGGCTCCTGTCACCCGGGG
139-145	consensus	CtTGGCCTCTTACGGCAATGAGGCTGTGGGCAAGGGTGGGGATGGCTCCTGTCACCCGGGG	145	306	CTCTCGGCCGTCTGGGGCCGAAATGATCCCCGGAGGTCTCCGCAACTTGGGTAAGGTC
			143	306	CTCTCGACCGTCTGGGGCCAAATGATCCCCGGAGGTCTCCGCAACTTGGGTAAGGTC
			144	306	CTCTCGACCGTCTGGGGCCAAATGATCCCCGGAGGTCTCCGCAACTTGGGTAAGGTC
			140	306	CTCTCGACCGTCTGGGGCCAAATGATCCCCGGAGGTCTCCGCAACTTGGGTAAGGTC
			139	306	CTCTGGCCATCTGGGGCCAAATGATCCCCGGAGGTCTCCGCAACTTGGGTAAGGTC
			142	306	aTCTGGCCATCTGGGGCCAAATGATCCCCGGAGGTCTCCGCAACTTGGGTAAGGTC
			141	306	tTcaGGCCgtCTGGGGCCAAATGATCCCCGGAGGTCTCCGCAACTTGGGTAAGGTC
139-145	consensus	ctCTCGGCCgtCTGGGGCCAAATGATCCCCGGAGGTCTCCGCAACTTGGGTAAGGTC			

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1...

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FIGURE 6H-3

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF

THE ENVELOPE 1...

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FIGURE 6H-4

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
145	DK13	550 TGCCTgACTGTTCCCGCTTGGCC
143	Z6	550 TGCCCTAACGTGTTCCACCTCGGCC
144	Z7	550 TGCCCTAACGTGTTCCAGCCTCGGCC
140	Z8	550 TGCCCTAACCGGTCCAGGTCCTGCT
139	Z4	550 TGCCCTAACGTtCCAGGTCGGCT
142	Z5	550 TGCTTGACAACACCAGCATCCGCT
141	Z1	550 TGCTTGACAACACCAGCATCTGCC
139-145	consensus	TGCCTgACTgttcc-gc-TGggcc

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6I-1

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
153	SA11	1 ATGAGCACCGAATCCTAAACCTCAAGAAAAACCCaaAAAAGAAACACCAAAACCCGGCCACAGG
152	SA6	1 ATGAGCACCGAATCCTAAACCTCAAGAAAAACCCaaAAAAGAAACACCAAAACCCGGCCACAGG
146	SA4	1 ATGAGCACCGAATCCTAAACCTCAAGAAAAACCCaaAAAAGAAACACCAAAACCCGGCCACAGG
147	SA5	1 ATGAGCACCGAATCCTAAACCTCAAGAAAAACCCaaAAAAGAAACACCAAAACCCGGCCACAGG
148	SA7	1 ATGAGCACCGAATCCTAAACCTCAAGAAAAACCCaaAAAAGAAACACCAAAACCCGGCCACAGG
149	SA1	1 ATGAGCACCGAATCCTAAACCTCAAGAAAAACCCaaAAAAGAAACACCAAAACCCGGCCACAGG
150	SA3	1 ATGAGCACCGAATCCTAAACCTCAAGAAAAACCCaaAAAAGAAACACCAAAACCCGGCCACAGG
151	SA13	1 ATGAGCACCGAATCCTAAACCTCAAGAAAAACCCaaAAAAGAAACACCAAAACCCGGCCACAGG
146-153	consensus	ATGAGCACCGAATCCTAAACCTCAAGAAAAACCCaaAAAAGAAACACCAAAACCCGGCCACAGG
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
153	SA11	62 AGCTCAAGTCCGGGGGGGTCAAGTCGTTGGAGTTTACTTGTGCCGGCAGGGG
152	SA6	62 AGCTCAAGTCCGGGGGGGTCAAGTCGTTGGAGTTTACTTGTGCCGGCAGGGG
146	SA4	62 AGCTCAAGTCCGGGGGGGTCAAGTCGTTGGAGTTTACTTGTGCCGGCAGGGG
147	SA5	62 AGCTCAAGTCCGGGGGGGTCAAGTCGTTGGAGTTTACTTGTGCCGGCAGGGG
148	SA7	62 AGCTCAAGTCCGGGGGGGTCAAGTCGTTGGAGTTTACTTGTGCCGGCAGGGG
149	SA1	62 AGCTCAAGTCCGGGGGGGTCAAGTCGTTGGAGTTTACTTGTGCCGGCAGGGG
150	SA3	62 AGCTCAAGTCCGGGGGGGTCAAGTCGTTGGAGTTTACTTGTGCCGGCAGGGG
151	SA13	62 AGCTCAAGTCCGGGGGGGTCAAGTCGTTGGAGTTTACTTGTGCCGGCAGGGG
146-153	consensus	ACGTCAAGTCCGGGGGGGTCAAGTCGTTGGAGTTTACTTGTGCCGGCAGGGG
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
153	SA11	123 CCCTaGgtTGGGTGCGCGGACTCGGAAGAACGACTCGTAAGAACCCCGTGGGCGG
152	SA6	123 CCCTCGtaTGGGTGCGCGGACTCGGAAGAACGACTCGTAAGAACCCCGTGGGCGG
146	SA4	123 CCCTAGgtTGGGTGCGCGGACTCGGAAGAACGACTCGTAAGAACCCCGTGGGCGG
147	SA5	123 CCCTAGtaTGGGTGCGCGGACTCGGAAGAACGACTCGTAAGAACCCCGTGGGCGG
148	SA7	123 CCCTAGgtTGGGTGCGCGGACTCGGAAGAACGACTCGTAAGAACCCCGTGGGCGG
149	SA1	123 CCCTAGgtTGGGTGCGCGGACTCGGAAGAACGACTCGTAAGAACCCCGTGGGCGG
150	SA3	123 CCCTAGgtTGGGTGCGCGGACTCGGAAGAACGACTCGTAAGAACCCCGTGGGCGG
151	SA13	123 CCCTAGgtTGGGTGCGCGGACTCGGAAGAACGACTCGTAAGAACCCCGTGGGCGG
146-153	consensus	CCCTaGgtTGGGTGCGCGGACTCGGAAGAACGACTCGTAAGAACCCCGTGGGCGG

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FIGURE 6I-2

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
153	SA11	184 CGTCAGCCTATTCCCAAGGCGGCCAACCAACGGGCCATCCCGGGTCAACCCGGGTACCC
152	SA6	184 CGTCAGCCTATTCCCAAGGCGGCCAACCAACGGGCCATCCCGGGTCAACCCGGGTACCC
146	SA4	184 CGCCAGCCTATTCCCAAGGCGGCCAACCAACGGGCCATCCCGGGTCAACCCGGGTACCC
147	SA5	184 CGCCAGCCTATTCCCAAGGCGGCCAACCAACGGGCCATCCCGGGTCAACCCGGGTACCC
148	SA7	184 CGCCAGCCTATTCCCAAGGCGGCCAACCAACGGGCCATCCCGGGTCAACCCGGGTACCC
149	SA1	184 CGCCAGCCTATTCCCAAGGCGGCCAACCAACGGGCCATCCCGGGTCAACCCGGGTACCC
150	SA3	184 CGCCAGCCTATTCCCAAGGCGGCCATCCCGGGTCAACCCGGGTACCC
151	SA13	184 CGTCAGCCTATTCCCAAGGCGGCCATCCCGGGTCAACCCGGGTACCC
146-153	consensus	CGCCAGCCTATTCCCAAGGCGGCCAACCAACGGGCCATCCCGGGTCAACCCGGGTACCC
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
153	SA11	245 CTTGGCCCTTTAACGCCAATGAGGGCCTCGGGTGGCAAGGGCTGGCTGGCTCTCCCCCTGGGG
152	SA6	245 CTTGGCCCTTTAACGCCAATGAGGGCCTCGGGTGGCAAGGGCTGGCTGGCTCTCCCCCTGGGG
146	SA4	245 CTTGGCCCTTTAACGCCAATGAGGGCCTCGGGTGGCAAGGGCTGGCTGGCTCTCCCCCTGGGG
147	SA5	245 CTTGGCCCTTTAACGCCAATGAGGGCCTCGGGTGGCAAGGGCTGGCTGGCTCTCCCCCTGGGG
148	SA7	245 CTTGGCCCTTTAACGCCAATGAGGGCCTCGGGTGGCAAGGGCTGGCTGGCTCTCCCCCTGGGG
149	SA1	245 CTTGGCCCTTTAACGCCAATGAGGGCCTCGGGTGGCAAGGGCTGGCTGGCTCTCCCCCTGGGG
150	SA3	245 CTTGGCCCTTTAACGCCAATGAGGGCCTCGGGTGGCAAGGGCTGGCTGGCTCTCCCCCTGGGG
151	SA13	245 CTTGGCCCTTTAACGCCAATGAGGGCCTCGGGTGGCAAGGGCTGGCTGGCTCTCCCCCTGGGG
146-153	consensus	CTTGGCCCTTTAACGCCAATGAGGGCCTCGGGTGGCAAGGGCTGGCTGGCTCTCCCCCTGGGG
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
153	SA11	306 CTCTCGGCCTAAACTGGGGCCCAATGACCCCCGGGAAGATCGGCGAACATTGGGCAAGGGTC
152	SA6	306 CTCTCGGCCTAAATTGGGGCCCAATGACCCCCGGGAAGATGGGTAAGGGTC
146	SA4	306 CTCTCGGCCTAAATTGGGGCCCAATGACCCCCGGGAAGATGGGTAAGGGTC
147	SA5	306 CTCTCGGCCTAAATTGGGGCCCAATGACCCCCGGGAAGATGGGTAAGGGTC
148	SA7	306 CTCTCGGCCTAAATTGGGGCCCAATGACCCCCGGGAAGATGGGTAAGGGTC
149	SA1	306 CTCTCGGCCTAAATTGGGGCCCAATGACCCCCGGGAAGATGGGTAAGGGTC
150	SA3	306 CTCTCGGCCTAATTGGGGCCCAACGACCCCCGGGAAGATGGGTAAGGGTC
151	SA13	306 CTCTCGGCCTAATTGGGGCCCAATGACCCCCGGGAAGATGGGTAAGGGTC
146-153	consensus	CTCTCGGCCTAAATTGGGGCCCAATGACCCCCGGGAAGATGGGTAAGGGTC

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1...

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FIGURE 6I-3

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6I-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
153	SA11	550 TGCTTgACCGGTCCCggCCaCTGCA
152	SA6	550 TGCCTtaACCGGTCCCTGCCCTTGCA
146	SA4	550 TGCCTrGACCGGTCCCggCCCTTGCA
147	SA5	550 TGCTTgACCGGTCCCAGCCTCTGCA
148	SA7	550 TGCCTGACCGGTCCCAGCCTCCGCA
149	SA1	550 TGTCTGATCATCCCCGGCCTCTGCA
150	SA3	550 TGCCTrGACCGGTCCCggCCCTCTGCA
151	SA13	550 TGCCTGACTGTCCCGac CCTCTGCC
146-153	consensus	TGccTgAccgtTCCCggCCtCTGCC

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF

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FIGURE 6J-1

<u>SEQ ID NO:</u>	<u>Genotype</u>	
103-154	cons.	1 ATGAGGCACgaaTCCTAAACCTCAAAGAAaACCAaACGTAAACACCAaCCgcGCCCaacagg
103-124	1	1 ATGAGGCACgAAatCCTAAACCTCAAAGAAaACCAaACGTAAACACCAaCCGCGCCCCAcacgg
125-134	2	1 ATGAGGCACAAarCCTAAACCTCAAAGAAaACCAaACGTAAACACCAaACGGCGCCCCAcagg
135-138	3	1 ATGAGGCACACTTCCTAAACCTCAAAGAAaACCAaACGTAAACACCAATCGTGCGCCAcagg
139-145	4	1 ATGAGGCACgAAATCCTAAACCTCAAAGAAaACCAaACGTAAACACCAACGGCGCCCCAcagg
146-153	5	1 ATGAGGCACgAAATCCTAAACCTCAAAGAAaACCAaACGTAAACACCAACGGCGCCCCAcagg
154	6	1 ATGAGGCACACTTCCTAAACCTCAAAGAAaACCAaACGTAAACACCAACGGCGCCCCAcagg
<u>SEQ ID NO:</u>	<u>Genotype</u>	
103-154	cons.	62 AcgtcaAGTTCCCGGGtGGtCAGATCGTtGGtGGAGTTACTTGTGCGCGAAGGG
103-124	1	62 ACgtcaAGTTCCGGGGGGtGGtCAGATCGTtGGtGGAGTTACTTGTGCGCGAAGGG
125-134	2	62 ACgtcaAGTTCCGGGGGGtGGtCAGATCGTtGGtGGAGTTACTTGTGCGCGAAGGG
135-138	3	62 ACgtcaAGTTCCGGGGGGtGGtCAGATCGTtGGtGGAGTTACTTGTGCGCGAAGGG
139-145	4	62 ACgtcaAGTTCCGGGGGGtGGtCAGATCGTtGGtGGAGTTACTTGTGCGCGAAGGG
146-153	5	62 ACgtcaAGTTCCGGGGGGtGGtCAGATCGTtGGtGGAGTTACTTGTGCGCGAAGGG
154	6	62 ACgtcaAGTTCCGGGGGGtGGtCAGATCGTtGGtGGAGTTACTTGTGCGCGAAGGG
<u>SEQ ID NO:</u>	<u>Genotype</u>	
103-154	cons.	123 CCCcaGgtTGGGTGCGCggaCtaGgAAgactTCCGTCGAAccTcGtGGAaGg
103-124	1	123 CCCcaGgtTGGGTGCGCgactAGGAAAGACTTCCGAGGGTGCAACCTCGtGGAaGg
125-134	2	123 CCCcaGgtTGGGTGCGCgACAAAGGAAGACTTCCGAGGGTGCAACCTCGtGGAaGg
135-138	3	123 CCCACGATTTGGGTGCGCgACGGTAaaaACTTCTGAACGGTcaAGGCCCTCGGGACGA
139-145	4	123 CCCcaGgtTGGGTGCGCgactCGgAAAGACTTCCGAGGGTGCAACCTCGtGGAaGg
146-153	5	123 CCCcaGgtTGGGTGCGCgACTCGGAAAGACTTCCGAGGGTGCAACCTCGtGGAaGg
154	6	123 CCCcaGgtTGGGTGCGCgACTCGGAAAGACTTCCGAGGGTGCAACCTCGtGGAaGg

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1...

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FIGURE 6J-2

<u>SEQ_ID</u>	<u>ID NO:</u>	<u>Genotype</u>	<u>cons.</u>
103-154		CGaCAGGCCATGCCcaAgGctCGcCggcccgagGGcaggCCCTGGGtcagCCGGgtACC	184
103-124	1	CGaCACCTATCCCAGGCTCGCCGGCCGGAGGGAGGGCTAGCCCCGGGTAC	184
125-134	2	CGCCAGGCCATCCGAAGATCGGGCTCACTGGAAAGCTGGGAAaccAGGATACT	184
135-138	3	CGACAGCCATCCCAAGGGCGTGGAGCGAAGGCCGGTCCAGGCCGGTAC	184
139-145	4	CGtCAGGCCATCCCAAGGCaCGtCggtCCGAGGAGGCTAGGCCGGTAC	184
146-153	5	CGCCAGGCCATTCCCAAGGGCGGCCAACCCAcGGGCCGGTCCAGGCCACTGGGCTACGCCGGATACC	184
154	6	CGCCAAACCTATACCAAGGGGCCAGGCCAGGGCAGGCACGGCAGGGTAC	184
<u>SEQ_ID</u>	<u>ID NO:</u>	<u>Genotype</u>	<u>cons.</u>
103-154		CtTG GCCC CTC TAtGgccaAtGAGG GtttCggTGGCcaggTaGGCTCCTgtTCCC CGGG	245
103-124	1	CtTG GCCC CTC TAtGgCaAtGAGG GtttCggTGGCcaggTaGGCTCCTgtTAcCCCCGtGG	245
125-134	2	CtTG GCCC CTC TAtGgGaAtGAGG GtttCggTGGCcaggTGGCTCCTgtTCCCCGGGG	245
135-138	3	CtTG GCCC CTC TAtGgTAACGAGG GCTGGGTGGCTGGCTGGGCTGGGAGGGTGGCTCCTgtTCCCCGGGG	245
139-145	4	CtTG GCCC CTC TAtGgCAAtGAGG GtttCggTGGCcaggTaGGCTGGGAGGGTGGCTGGGAGGGTGGCTCCTgtTCCCCGGGG	245
146-153	5	CtTG GCCC CTC TAtGgCCAAtGAGG GtttCggTGGCcaggTaGGCTGGGAGGGTGGCTGGGAGGGTGGCTCCTgtTCCCCGGGG	245
154	6	CtTG GCCC CTC TAtGgAAACGAGG GCTGGGAGGGTGGCTGGGAGGGTGGCTCCTgtTCCCCGGGG	245
<u>SEQ_ID</u>	<u>ID NO:</u>	<u>Genotype</u>	<u>cons.</u>
103-153		cTCTcggGCCtagtTGGGCCActGACCCCCGGCtagggTcgcgcAAattTGGGtaaggTc	306
103-124	1	cTCTcggGCCtagtTGGGCCActGACCCCCGGCtagggTcgcgcAAattTGGGtaaggTc	306
125-134	2	tTCTcgtCtttCtTGGGCCCAactGACCCCCGGCtagggTcgcgcAAattTGGGtaaggTc	306
135-138	3	CTCCCGTCatCTTGGGCCAAACGACCCCCGGCtagggTcgcgcAAattTGGGtaaggTc	306
139-145	4	CTCTcggCCgtCTTGGGCCAAATGATCCGGGCAAAATGATCCGGGCAAGGTTGGGtaaggTc	306
146-153	5	CTCTcggGCCtaatTGGGCCAAATGACCCCCGGCAGGGTGGCTGGGAGGGTGGCTCCTgtTCCCCGGGG	306
154	6	CTCCCGGGCAGATGGGCCAAATGACCCCCGGCAGGGTGGCTGGGAGGGTGGCTCCTgtTCCCCGGGG	306

NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6J-3

<u>SEQ ID NO:</u>	<u>Genotype</u>	
103-154	cons.	367 ATCGATAACCCCTcACgTGCggGctTCGCCGACCTCATGGGTACATCCCgtCTGTCGGCGCCC
103-124	1	367 ATCGATAACCCCTcACATGCGGCTTcGCCGACCTCATGGGTACATCCCgtCTGTCGGCGCCC
125-134	2	367 ATCGATAACCCCTaACgTGCggGttTTGCCGACCTCATGGGTACATCCCgtCTGTCGGCGCCC
135-138	3	367 ATCGATAACCCCTtACGTGGGAtTTGCCGACCTCATGGGTACATCCCgtCTGTCGGCGCCC
139-145	4	367 ATCGATAACCCCTgACgTGCggGttTGCggGACCTCATGGGTACATCCCgtCTGTCGGCGCCC
146-153	5	367 ATCGATAACCCCTaACgTGCggGAtTTGCCGACCTCATGGGTACATCCCgtCTGTCGGCGCCC
154	6	367 ATCGATAACCCCTAACGTGTGGGTTGCCGATCTCATGGGTACATCCCgtCTGTCGGCGCCC
<u>SEQ ID NO:</u>	<u>Genotype</u>	
103-154	cons.	428 CcgTagGggGGGtCGCcaggGGCCCTggGgcATGGcGtcaGggttcTgGAGGACGGGgtGAA
103-124	1	428 CccTagGggGGGCGTGCAGGCCCCCTggGgtGGGgtCCTGGGAGGACGGGgtGAA
125-134	2	428 CggGttGGAGGGCGTGCAGGCCCCCTggGgtGGGAGGACGGGgtGAA
135-138	3	428 CCGTAGGAGGGCGTGCAGGCCCCCTGGGAGGACGGGgtGAA
139-145	4	428 CCGTggGtGGGGGCGTGCAGGCCCCCTggGgtGGGAGGACGGGgtGAA
146-153	5	428 CCGTTGGGGGGCGTGCAGGCCCCCTGGGAGGACGGGgtGAA
154	6	428 CTTTGGGGGGCGTGCAGGCCCCCTggGgtGGGAGGACGGGgtGAA
<u>SEQ ID NO:</u>	<u>Genotype</u>	
103-154	cons.	489 cTatGCAACAGGAAttTgCCCGGGTTGctCTTtCtATCTTCCtGgtcTgtgtGCC
103-124	1	489 CTATGCAACAGGAAttTgCCCGGGTTGctCTTtCtATCTTCCtGgtcTgtgtGCC
125-134	2	489 TTATGCAACAGGAAttTgCCCGGGTTGctCTTtCtATCTTCCtGgtcTgtgtGCC
135-138	3	489 TTTCGCAACAGGAActTGCCTGGGTTGctCTTtCtATCTTCCtGgtcTgtgtGCC
139-145	4	489 CTATGCAACAGGAActTGCCTGGGTTGctCTTtCtATCTTCCtGgtcTgtgtGCC
146-153	5	489 CTATGCAACAGGAAttTgCCCGGGTTGctCTTtCtATCTTCCtGgtcTgtgtGCC
154	6	489 TTATGCAACAGGAAttTCCCGGGTTGctCTTtCtATCTTCCtGgtcTgtgtGCC

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FIGURE 6J-4

<u>SEQ ID NO:</u> 103-154	<u>Genotype</u> cons.	550	TGccTgaccgttCCAgcttCtgct
103-124	1	550	TGTTgACCATCCAGcttCCGGCT
125-134	2	550	TGCatCAAGtGCCAGtGTCTGCT
135-138	3	550	TGCTTAATTCAATCCAGCAAGCTAGT
139-145	4	550	TGCCCTgACTgttCCAGGCCGTCGGCC
146-153	5	550	TGCCTgACCgtTCCCggCCtCTGCA
154	6	550	TGCCTCACAAACGCCAGCTTGGCT

*NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
THE ENVELOPE 1...*

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FIGURE 6K-1

SEQ ID NO:	Genotype	SEQ ID NO:	Genotype	SEQ ID NO:	Genotype
103-108	I/1a	103-108	I/1a	103-108	I/1a
109-124	I/1b	109-124	I/1b	109-124	I/1b
125-128	III/2a	125-128	III/2a	125-128	III/2a
129-133	IV/2b	129-133	IV/2b	129-133	IV/2b
134	2c	134	2c	134	2c
135-138	(V)/3a	135-138	(V)/3a	135-138	(V)/3a
139	4a	139	4a	139	4a
141	4b	141	4b	141	4b
143	4c	143	4c	143	4c
145	4d	145	4d	145	4d
146	4e	146	4e	146	4e
146-153	4f	146-153	4f	146-153	4f
154	5a	154	5a	154	5a
6a	6a	6a	6a	6a	6a
10	ATGAGCACGaa	10	ATGAGCACGaa	10	ATGAGCACGaa
20	TCCAAACC	20	TCCAAACC	20	TCCAAACC
30	CAAGA	30	CAAGA	30	CAAGA
40	ACACCA	40	ACACCA	40	ACACCA
50	CCGCC	50	CCGCC	50	CCGCC
60	caAGG	60	caAGG	60	caAGG
70	GGG	70	GGG	70	GGG
80	GGG	80	GGG	80	GGG
90	GGG	90	GGG	90	GGG
100	GGG	100	GGG	100	GGG
110	GGG	110	GGG	110	GGG
120	GAA	120	GAA	120	GAA
130	AA-	130	AA-	130	AA-
140	AA-C-T	140	AA-C-T	140	AA-C-T
150	-AA-C-T	150	-AA-C-T	150	-AA-C-T
160	-AA-C-T	160	-AA-C-T	160	-AA-C-T
170	-AA-C-T	170	-AA-C-T	170	-AA-C-T
180	-AA-C-T	180	-AA-C-T	180	-AA-C-T
190	-AA-C-T	190	-AA-C-T	190	-AA-C-T
200	-AA-C-T	200	-AA-C-T	200	-AA-C-T
210	-AA-C-T	210	-AA-C-T	210	-AA-C-T
220	-AA-C-T	220	-AA-C-T	220	-AA-C-T
230	-AA-C-T	230	-AA-C-T	230	-AA-C-T
240	TA-AT	240	TA-AT	240	TA-AT
250	-CA-GT	250	-CA-GT	250	-CA-GT
260	-CA-GT	260	-CA-GT	260	-CA-GT
270	-CA-GT	270	-CA-GT	270	-CA-GT
280	-CA-GT	280	-CA-GT	280	-CA-GT
290	-CA-GT	290	-CA-GT	290	-CA-GT
300	-CA-GT	300	-CA-GT	300	-CA-GT
310	-CA-GT	310	-CA-GT	310	-CA-GT
320	-CA-GT	320	-CA-GT	320	-CA-GT
330	-CA-GT	330	-CA-GT	330	-CA-GT
340	-CA-GT	340	-CA-GT	340	-CA-GT

**NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF
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FIGURE 6K-2

SEQ ID NO: Genotype	350	360	370	380	390	400	410	420	430	440	450	460
TcgGcAatTGGtAaggTCATGATAccCTcAgtGggctcGGGACCTCATGGGTACatccggcTGTcggccGccGGatcCaggGccCGtgccggGATGCGATC	-G-C-TT-t-Ag-----t-CC-C-G-t-G-C-T-C-----C-----G-A-a-GC-----C-C-C-a-C-CT-----CAGG-----CC-G-G-T-----											
I/1a	-G-t-Tt-T-Ag-----t-CC-C-G-t-G-C-T-C-----C-----G-A-t-GC-----C-C-C-A-G-C-C-T-----CAGG-----CC-G-g-T-----											
I/1b	-G-C-G-T-Ag-----t-CC-A-G-C-G-C-T-----C-----G-a-C-G-----B-D-C-G-C-t-T-C-C-A-G-C-T-----CAGA-----TG-C-G-T-----											
I/1/2a	-A-C-TT-c-aa-----C-CA-T-g-----TG-TT-T-----C-----G-A-TG-----T-C-CC-GG-C-A-C-T-C-----CAGA-----TG-G-A-C-----											
IV/2b	-G-C-CT-T-AG-----T-CC-A-G-C-G-C-T-----C-----G-A-A-CG-----T-C-C-T-C-G-T-C-C-C-T-----CAGA-----TG-C-G-T-----											
2c	-C-C-TT-T-Aa-----T-CC-t-G-CG-AT-C-----C-----G-A-C-GC-----C-C-CT-CG-A-a-C-T-C-----CAGA-----TG-C-G-T-----											
(V)/3a	-G-C-Tc-T-Ag-----T-CC-G-G-CG-C-T-C-----C-----G-C-CG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
4a	-C-T-Tc-T-AA-----T-CC-G-G-CG-C-T-C-----C-----G-A-A-C-GA-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
4b	-C-C-Ct-T-AG-----T-CC-A-t-CG-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
4c	-C-C-Ct-T-AG-----T-CC-A-t-CG-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
4d	-C-C-Ct-T-AG-----T-CC-A-t-CG-T-C-----C-----G-A-A-C-GA-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
4f	-C-C-Ct-T-AG-----T-CC-C-G-CG-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
5a	-G-C-TT-t-AG-----t-CC-a-g-CG-AT-C-----C-----G-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
115	-C-G-TT-T-AG-----t-CC-A-G-TG-C-T-C-----C-----G-A-t-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
116	-C-C-C-T-----C-----G-C-G-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
117	-G-C-TT-T-AG-----t-CC-C-G-CG-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
118	-G-C-TT-t-AG-----t-CC-a-g-CG-AT-C-----C-----G-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
119	-C-G-TT-T-AG-----t-CC-A-G-TG-C-T-C-----C-----G-A-t-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
120	-C-C-C-T-----C-----G-C-G-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
121	-G-C-TT-T-AG-----t-CC-C-G-CG-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
122	-G-C-TT-t-AG-----t-CC-a-g-CG-AT-C-----C-----G-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
123	-C-G-TT-T-AG-----t-CC-A-G-TG-C-T-C-----C-----G-A-t-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
124	-C-C-C-T-----C-----G-C-G-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
125	-G-C-TT-T-AG-----t-CC-C-G-CG-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
126	-G-C-TT-t-AG-----t-CC-a-g-CG-AT-C-----C-----G-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
127	-C-G-TT-T-AG-----t-CC-A-G-TG-C-T-C-----C-----G-A-t-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
128	-C-C-C-T-----C-----G-C-G-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
129	-G-C-TT-T-AG-----t-CC-C-G-CG-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
133	-G-C-TT-t-AG-----t-CC-a-g-CG-AT-C-----C-----G-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
134	-C-G-TT-T-AG-----t-CC-A-G-TG-C-T-C-----C-----G-A-t-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
135	-C-C-C-T-----C-----G-C-G-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
138	-G-C-TT-T-AG-----t-CC-C-G-CG-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
139	-G-C-TT-t-AG-----t-CC-a-g-CG-AT-C-----C-----G-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
141	-C-G-TT-T-AG-----t-CC-A-G-TG-C-T-C-----C-----G-A-t-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
142	-C-C-C-T-----C-----G-C-G-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
143	-G-C-TT-T-AG-----t-CC-C-G-CG-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
144	-G-C-TT-t-AG-----t-CC-a-g-CG-AT-C-----C-----G-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
145	-C-G-TT-T-AG-----t-CC-A-G-TG-C-T-C-----C-----G-A-t-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
146	-C-C-C-T-----C-----G-C-G-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
153	-G-C-TT-T-AG-----t-CC-C-G-CG-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGG-----TG-G-G-T-----											
154	-C-G-TT-T-AG-----t-CC-A-G-TG-C-T-C-----C-----G-A-t-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											
155	-C-C-C-T-----C-----G-C-G-C-T-C-----C-----G-A-A-C-GC-----A-C-CC-GG-C-G-C-T-C-----CAGA-----TG-G-G-T-----											

FIGURE 7A-1

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
156	US11	MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLP芮RGPRILGVRATRKTTSERSQPRGR
157	S14	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLP芮RGPRILGVRATRKTTSERSQPRGR
158	SW1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLP芮RGPRILGVRATRKTTSERSQPRGR
159	S18	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLP芮RGPRILGVRATRKTTSERSQPRGR
160	DR4	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLP芮RGPRILGVRATRKTTSERSQPRGR
155	DK7	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLP芮RGPRILGVRATRKTTSERSQPRGR
155-160	consensus	MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLP芮RGPRILGVRATRKTTSERSQPRGR
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
156	US11	RQPIPKARRPEGRRTWAQPGYPWPPLYNEGGCWAGWILLSPRGSRPSWGPTDPRRSRNLGKV
157	S14	62 RQPIPKARRPEGRRTWAQPGYPWPPLYNEGGCWAGWILLSPRGSRPSWGPTDPRRSRNLGKV
158	SW1	62 RQPIPKARRPEGRRTWAQPGYPWPPLYNEGGCWAGWILLSPRGSRPSWGPTDPRRSRNLGKV
159	S18	62 RQPIPKARRPEGRRTWAQPGYPWPPLYNEGGCWAGWILLSPRGSRPSWGPTDPRRSRNLGKV
160	DR4	62 RQPIPKARRPEGRRTWAQPGYPWPPLYNEGGCWAGWILLSPRGSRPSWGPTDPRRSRNLGKV
155	DK7	62 RQPIPKARRPEGRRTWAQPGYPWPPLYNEGGCWAGWILLSPRGSRPSWGPTDPRRSRNLGKV
155-160	consensus	RQPIPKARRPEGRRTWAQPGYPWPPLYNEGGCWAGWILLSPRGSRPSWGPTDPRRSRNLGKV
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
156	US11	IDTLTCGFADLMGYIPLVGAPLGAARALAHGVRLLEDGVNYATGNLPGCSFSIFLLALLS
157	S14	123 IDTLTCGFADLMGYIPLVGAPLGAARALAHGVRLLEDGVNYATGNLPGCSFSIFLLALLS
158	SW1	123 IDTLTCGFADLMGYIPLVGAPLGAARALAHGVRLLEDGVNYATGNLPGCSFSIFLLALLS
159	S18	123 IDTLTCGFADLMGYIPLVGAPLGAARALAHGVRLLEDGVNYATGNLPGCSFSIFLLALLS
160	DR4	123 IDTLTCGFADLMGYIPLVGAPLGAARALAHGVRLLEDGVNYATGNLPGCSFSIFLLALLS
155	DK7	123 IDTLTCGFADLMGYIPLVGAPLGAARALAHGVRLLEDGVNYATGNLPGCSFSIFLLALLS
155-160	consensus	IDTLTCGFADLMGYIPLVGAPLGAARALAHGVRLLEDGVNYATGNLPGCSFSIFLLALLS

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FIGURE 7A-2

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
156	US11	184 CLTPASA
157	S14	184 CLTPASA
158	SW1	184 CLTPASA
159	S18	184 CLTPASA
160	DR4	184 CLTPASA
155	DK7	184 CLTPASA
155-160	consensus	CLTPASA

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FIGURE 7B-1

<u>SEQ</u>	<u>ID NO.</u>	<u>ISOLATE</u>
175	P8	IND8
170	S45	
162	S9	
171	D1	
163	P10	
165	IND3	
169	US6	
164	DK1	
166	T10	
167	SW2	
168	SA10	
161	HK4	
174	HK3	
172	T3	
176	HK5	
173		

ROPIPKAREPEGRaWAQOPGYPWPBLXanEG-GWAGWLLSPRGSRPSWGPTDPRRRBSRNLGKV

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FIGURE 7B-2

SEQ	ID NO:	ISOLATE	175	170	162	171	S45	S9	D1	P10	IND3	US6	DK1	T10	SW2	SA10	HK4	HK3	T3	HK5			
123	P8		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	IND8		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	S45		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	S9		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	D1		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	P10		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	IND3		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	US6		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	DK1		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	T10		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	SW2		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	SA10		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	DF	S	IF	FL	LL
123	HK4		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	HK3		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	T3		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL
123	HK5		IDT	TCG	FAD	LMGY	IPLV	G	PLG	GVA	RALA	HGV	V	EDG	VNY	ATG	NL	PGC	SFS	IF	FL	LL	LL

SEQ_ID_NO:	ISOLATE	161-176	consensus	IDTLCGFADLMGYIPLVCGaPLGGaARRALAHGVRVIEDGVNYATGNIPGCsFSIFLLALLS
175	P8	184	CLTiPASA	
170	IND8	184	CLTiPASA	
162	S45	184	CLTiPASA	
171	S9	184	CLTiPASA	
163	D1	184	CLTiPASA	
165	P10	184	CLTiPASA	
169	IND3	184	CLTiPASA	
164	US6	184	CLTiPASA	
166	DK1	184	CLTiPASA	
167	T10	184	CLTiPASA	
168	SW2	184	CLTiPASA	
161	SA10	184	CLTiPASA	
174	HK4	184	CLTiPASA	
172	HK3	184	CLTiPASA	
176	T3	184	CLTiPASA	
173	HK5	184	CLTPvSA	
161-176	consensus			CLTiPASA

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FIGURE 7C-1

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
173	HK5	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
176	T3	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
172	HK3	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
174	HK4	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
161	SA10	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
168	SW2	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
167	T10	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
166	DK1	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
164	US6	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
169	IND3	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
165	P10	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
163	D1	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
156	US11	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
157	S14	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
158	SW1	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
159	S18	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
160	DR4	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
155	DK7	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
170	IND8	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
162	S45	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
171	S9	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
175	P8	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
155-176	consensus	

MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA
TRKTSERSQPRGR

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FIGURE 7C-2

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>		<u>consensus</u>
173	HK5	T3	1155-176
176		HK3	
172		HK4	
174	SA10	SW2	
161		T10	
168		DK1	
167		US6	
166		IND3	
164		P10	
169		D1	
165		US11	
163		S14	
156		SW1	
157		S18	
158		DR4	
159		DK7	
160		IND8	
155		S45	
170		S9	
162		P8	
171			
175			

ROPIPKARIPEGRAWAOPGYPWPWLYmEG-GWAGWLSPRGSRPSEGPTDPRRRSSRNLLGV

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FIGURE 7C-3

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
173	HK5	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
176	T3	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
172	HK3	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
174	HK4	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
161	SA10	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
168	SW2	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
167	T10	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
166	DK1	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
164	US6	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
169	IND3	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
165	P10	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
163	D1	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
156	US11	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
157	S14	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
158	SW1	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
159	S18	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
160	DR4	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
155	DK7	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
170	IND8	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
162	S45	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
171	S9	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
175	P8	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS
155-176	consensus	IDTLLTCGFADLMGYIPLVGAAPLGGAARALAHGVVRVLEDGVNAYATGN1PGCSFSIFILLALLS

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FIGURE 7C-4

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
173	HK5	184 CLTtPVSA
176	T3	184 CLTiPASA
172	HK3	184 CLTtPASA
174	HK4	184 CLTiPASA
161	SA10	184 CLTiPASA
168	SW2	184 CLTiPASA
167	T10	184 CLTiPASA
166	DK1	184 CLTiPASA
164	US6	184 CLTiPASA
169	IND3	184 CLTiPASA
165	P10	184 CLTiPASA
163	D1	184 CLTiPASA
156	US11	184 CLTVPASA
157	S14	184 CLTVPASA
158	SW1	184 CLTVPASA
159	S18	184 CLTVPASA
160	DR4	184 CLTVPASA
155	DK7	184 CLTVPASA
170	IND8	184 CLTVPASA
162	S45	184 CLTiPASA
171	S9	184 CLTiPASA
175	P8	184 CLTiPASA
155-176	consensus	CLTiPaSA

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FIGURE 7D

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
179	T9	1 MSTnPKPQRKT'RNTRNRRPDKVKEPGGQIVGGVYLLPRRGPRLGVRtTRKTTSERSQPRGR
178	US10	1 MSTnPKPQRKT'RNTRNRRPDKVKEPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
180	T2	1 MSTnPKPQRKT'RNTRNRRPDKVKEPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177	T4	1 MSTnPKPQRKT'RNTRNRRPDKVKEPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177-180	consensus	MSTnPKPQRKT'RNTRNRRPDKVKEPGGQIVGGVYLLPRRGPRLGVRatTRKTTSERSQPRGR
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
179	T9	62 RQPIPKDRRSTGKSWGKPGYPWPLYGNEGCLGWAGWLLSPRGSRSPSWGPSPDPRHRSRNVGKV
178	US10	62 RQPIPKDRRPTGKSWGKPGYPWPLYGNEGCLGWAGWLLSPRGSRSPSWGPSPDPRHRSRNVGKV
180	T2	62 RQPIPKDRRSTGKSWGKPGYPWPLYGNEGCLGWAGWLLSPRGSRSPSWGPSPDPRHRSRNVGKV
177	T4	62 RQPIPKDRRSTGKSWGKPGYPWPLYGNEGCLGWAGWLLSPRGSRSPSWGPSPDPRHRSRNVGKV
177-180	consensus	RQPIPKDRRSTGKSWGKPGYPWPLYGNEGCLGWAGWLLSPRGSRSPSWGPSPDPRHRSRNVGKV
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
179	T9	123 IDTlTCGFADLMGYiPVVGAPLGGVARALAHGVRYLEDGVNYATGNLPGCSFSIFLALLS
178	US10	123 IDTlTCGFADLMGYiPVVGAPLGGVARALAHGVRYLEDGVNYATGNLPGCSFSIFLALLS
180	T2	123 IDTlTCGFADLMGYiPVVGAPLGGVARALAHGVRYLEDGVNYATGNLPGCSFSIFLALLS
177	T4	123 IDTlTCGS1ADLMGYiPVVGFLGGVARALAHGVRYLEDGVNYATGNLPGCSFSIFLALLS
177-180	consensus	IDTlTCGFADLMGYiPVVGAPLGGVARALAHGVRYLEDGVNYATGNLPGCSFSIFLALLS
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
179	T9	184 CITIPvSA
178	US10	184 CITIPvSA
180	T2	184 CITIPvSA
177	T4	184 CITIPvSA
177-180	consensus	CITIPvSA

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FIGURE 7E

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
183	DK11	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPQQGPRLGVRTTRKTSERSQPRGR
184	SW3	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPQQGPRLGVRTTRKTSERSQPRGR
181	T8	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPQQGPRLGVRTTRKTSERSQPRGR
182	US1	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPQQGPRLGVRTTRKTSERSQPRGR
185	DK8	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPQQGPRLGVRTTRKTSERSQPRGR
181-185	consensus	MSTNPKPQRTKRNTRPQDVKFPGGGQIVGGVYLLPQQGPRLGVRTTRKTSERSQPRGR
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
183	DK11	RQPIPKDRRSTGKPGKPGWPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDBRHkSRNLGKV
184	SW3	RQPIPKDRRSTGKSWGKPGWPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDBRHRSRNLGKV
181	T8	RQPIPKDRRSTGKSWGKPGWPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDBRHRSRNLGKV
182	US1	RQPIPKDRRSTGKSWGKPGWPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDBRHRSRNLGKV
185	DK8	RQPIPKDRRSTGKSWGKPGWPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDBRHRSRNLGKV
181-185	consensus	RQPIPKDRRSTGKSWGKPGWPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDBRHRSRNLGKV
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
183	DK11	IDITITCGFADLMGYIPVVGAPVGGVARALAHGVRLIEDGINYATGNLPGCSFSIFLALLS
184	SW3	IDITITCGFADLMGYIPVVGAPVGGVARALAHGVRLIEDGINYATGNLPGCSFSIFLALLS
181	T8	IDITITCGFADLMGYIPVVGAPVGGVARALAHGVRLIEDGINYATGNLPGCSFSIFLALLS
182	US1	IDITITCGFADLMGYIPVVGAPVGGVARALAHGVRLIEDGINYATGNLPGCSFSIFLALLS
185	DK8	IDITITCGFADLMGYIPVVGAPVGGVARALAHGVRLIEDGINYATGNLPGCSFSIFLALLS
181-185	consensus	IDITITCGFADLMGYIPVVGAPVGGVARALAHGVRLIEDGINYATGNLPGCSFSIFLALLS
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
183	DK11	184 CCTVPVSA
184	SW3	184 CFTVPVSA
181	T8	184 CFTVPVSA
182	US1	184 CatVPVSA
185	DK8	184 CCTVPVSA
181-185	consensus	C-TVVPVSA

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FIGURE 7F-1

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FIGURE 7F-2

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	<u>SEQ ID NO:</u>	<u>ISOLATE</u>
183	DK11	183	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
184	SW3	184	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
181	T8	181	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
182	US1	182	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
185	DK8	185	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
186	S83	186	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
178	US10	178	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
180	T2	180	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
179	T9	179	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
177	T4	177	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
1177-186	consensus	1177-186	IDT-TCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFILLALLS
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	<u>SEQ ID NO:</u>	<u>ISOLATE</u>
183	DK11	183	CCTIPVSA
184	SW3	184	CFTIPVSA
181	T8	184	CFTIPVSA
182	US1	184	CATIPVSA
185	DK8	184	CCTIPVSA
186	S83	184	CISIPVSA
178	US10	184	CITIPVSA
180	T2	184	CITIPVSA
179	T9	184	CITIPasa
177	T4	184	CITIPvsa
1177-186	consensus	1177-186	CitIPVSA

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FIGURE 7G

<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
189	S2	
187	HK10	1 MSTLPKPORRKTKRNTIRRQD1KFPGGGQIVGGVYVLPRRGPRLLGVRA TRKTSERSORGR
190	DK12	1 MSTLPKPKQRKTKRNTIRRQDVKFPQDGKFPQGGQIVGGVYVLPRRGPRLLGVRA TRKTSERSORGR
188	S52	1 MSTLPKPKQRKTKRNTIRRQDVKFPQGGQIVGGVYVLPRRGPRLLGVRA TRKTSERSORGR
187-190	consensus	MSTLPKPKQRKTKRNTIRRQDVKFPQGGQIVGGVYVLPRRGPRLLGVRA TRKTSERSORGR
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
189	S2	RQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGCSRP SWGPNDPRRRSRMLGKV
187	HK10	62 RQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGCSRP SWGPNDPRRRSRMLGKV
190	DK12	62 RQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGCSRP SWGPNDPRRRSRMLGKV
188	S52	62 RQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGCSRP SWGPNDPRRRSRMLGKV
187-190	consensus	RQPIPKARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGCSRP SWGPNDPRRRSRMLGKV
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
189	S2	IDTLLTCGFADLMGYIPLVGAPVGGVARALAHGVRA LEDGINPATGNLPGCSFSIFILLALFS
187	HK10	123 IDTLLTCGFADLMGYIPLVGAPVGGVARALAHGVRA LEDGINPATGNLPGCSFSIFILLALFS
190	DK12	123 IDTLLTCGFADLMGYIPLVGAPVGGVARALAHGVRA LEDGINPATGNLPGCSFSIFILLALFS
188	S52	123 IDTLLTCGFADLMGYIPLVGAPVGGVARALAHGVRA LEDGINPATGNLPGCSFSIFILLALFS
187-190	consensus	IDTLLTCGFADLMGYIPLVGAPVGGVARALAHGVRA LEDGINPATGNLPGCSFSIFILLALFS
<u>SEQ ID NO.:</u>	<u>ISOLATE</u>	
189	S2	184 CLIHPAAS
187	HK10	184 CLIHPAAS
190	DK12	184 CLIHPAAS
188	S52	184 CLIHPAAS
187-190	consensus	CLIHPAAS

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FIGURE 7H-1

<u>SEQ</u>	<u>ID</u>	<u>NO:</u>	<u>ISOLATE</u>
	194		25
	193		Z1
	192		Z8
	195		Z6
	196		Z7
	191		Z4
	197		DK13
191-197			consensus
<u>SEQ</u>	<u>ID</u>	<u>NO:</u>	<u>ISOLATE</u>
	194		25
	193		Z1
	192		Z8
	195		Z6
	196		Z7
	191		Z4
	197		DK13
191-197			consensus

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FIGURE 7H-2

<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>	<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>
194		Z5	123	123	IDTLCGFADLMGYIPLVGA PVGGVARALAHGVRA LEDGINYATGNLPGCSFS SIFILLALLS
193		Z1	123	123	IDTLCGFADLMGYIPLVGA PVGGVARALAHGVRA LEDGINYATGNLPGCSFS SIFILLALLS
192		Z8	123	123	IDTLCGFADLMGYIPLVGA PVGGVARALAHGVRA LEDGINYATGNLPGCSFS SIFILLALLS
195		Z6	123	123	IDTLCGFADLMGYIPLVGA PVGGVARALAHGVRA LEDGINYATGNLPGCSFS SIFILLALLS
196		Z7	123	123	IDTLCGFADLMGYIPLVGA PVGGVARALAHGVRA LEDGINYATGNLPGCSFS SIFILLALLS
191		Z4	123	123	IDTLCGFADLMGYIPLVGA PVGGVARALAHGVRA LEDGINYATGNLPGCSFS SIFILLALLS
197		DK13	123	123	IDTLCGFADLMGYIPLVGA PVGGVARALAHGVRA LEDGINYATGNLPGCSFS SIFILLALLS
191-197		consensus			IDTLCGFADLMGYIPLVGA PVGGVARALAHGVRA LEDGINYATGNLPGCSFS SIFILLALLS
<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>	<u>SEQ_ID</u>	<u>ID_NO:</u>	<u>ISOLATE</u>
194		Z5	184	CLTPASA	
193		Z1	184	CLTPASA	
192		Z8	184	CLTPASA	
195		Z6	184	CLTPtSA	
196		Z7	184	CLTPASA	
191		Z4	184	CLTPASA	
197		DK13	184	CLTPASA	
191-197		consensus			CLTPASA

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FIGURE 7I-1

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
205	SA11	
202	SA3	
198	SA4	
199	SA5	
200	SA7	
203	SA13	
201	SA1	
204	SA6	
198-205	consensus	MSTINPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRILGVRA TRKTSERSOPRGR
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
205	SA11	
202	SA3	
198	SA4	
199	SA5	
200	SA7	
203	SA13	
201	SA1	
204	SA6	
198-205	consensus	RQPIPKARQOPTGRSWGQPGYPWPFYANEGGLGWAGWLSPRGSRPnWGPNDP RRkSRNLGKV

62	RQPIPKARQOPTGRSWGQPGYPWPFYANEGGLGWAGWLSPRGSRPnWGPNDP RRkSRNLGKV
62	RQPIPKARQsaGRSWGQPGYPWPFYANEGGLGWAGWLSPRGSRPnWGPNDP RRkSRNLGKV
62	RQPIPKARQsaGRSWGQPGYPWPFYANEGGLGWAGWLSPRGSRPnWGPNDP RRkSRNLGKV

RQPIPKARQOPTGRSWGQPGYPWPFYANEGGLGWAGWLSPRGSRPnWGPNDP
RRkSRNLGKV

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FIGURE 71-2

<u>SEQ ID NO:</u>	<u>ISOLATE</u>		
205	SA11	123	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRALEDGVNAYATGNLPGCFSFISIFILLALLS
202	SA3	123	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRLLEDGVNYATGNLPGCFSFISIFILLALLS
198	SA4	123	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRLLEDGVNYATGNLPGCFSFISIFILLALLS
199	SA5	123	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRLLEDGVNYATGNLPGCFSFISIFILLALLS
200	SA7	123	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRLLEDGVNYATGNLPGCFSFISIFILLALLS
203	SA13	123	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRLLEDGVNYATGNLPGCFSFISIFILLALLS
201	SA1	123	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRLLEDGVNYATGNLPGCFSFISIFILLALLS
204	SA6	123	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRLLEDGVNYATGNLPGCFSFISIFILLALLS
198-205	consensus		IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRLLEDGVNYATGNLPGCFSFISIFILLALLS
<u>SEQ ID NO:</u>	<u>ISOLATE</u>		
205	SA11	184	CLTVPA
202	SA3	184	CLTVPASA
198	SA4	184	CLTVPASA
199	SA5	184	CLTVPASA
200	SA7	184	CLTVPASA
203	SA13	184	CLTVPTSA
201	SA1	184	CLiiPASA
204	SA6	184	CLtvPASA
198-205	consensus		CLtvPasa

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FIGURE 7J

<u>SEQ ID NO:</u>	<u>Genotype</u>	
155-206	cons.	1 MSTLPKPKQRTKTKNTNRRPDKVFKPGCGGQIVYGGTYILPRRGPR1GVatrRKTTSERSQPRGRQPIPKarRpegrsWaqPgyPPWLYggGCCWAGW
155-176	type 1	MSTLPKPKQRTKTKNTNRRPDKVFKPGCGGQIVYGGTYILPRRGPR1GVatrRKTTSERSQPRGRQPIPKarRpegrsWaqPgyPPWLYggGCCWAGW
177-186	type 2	MSTLPKPKQRTKTKNTNRRPDKVFKPGCGGQIVYGGTYILPRRGPR1GVatrRKTTSERSQPRGRQPIPKarRpegrsWaqPgyPPWLYggGCCWAGW
187-190	type 3	MSTLPKPKQRTKTKNTNRRPDKVFKPGCGGQIVYGGTYILPRRGPR1GVatrRKTTSERSQPRGRQPIPKarRpegrsWaqPgyPPWLYggGCCWAGW
191-197	type 4	MSTLPKPKQRTKTKNTNRRPDKVFKPGCGGQIVYGGTYILPRRGPR1GVatrRKTTSERSQPRGRQPIPKarRpegrsWaqPgyPPWLYggGCCWAGW
198-205	type 5	MSTLPKPKQRTKTKNTNRRPDKVFKPGCGGQIVYGGTYILPRRGPR1GVatrRKTTSERSQPRGRQPIPKarRpegrsWaqPgyPPWLYggGCCWAGW
206	type 6	MSTLPKPKQRTKTKNTNRRPDKVFKPGCGGQIVYGGTYILPRRGPR1GVatrRKTTSERSQPRGRQPIPKarRpegrsWaqPgyPPWLYggGCCWAGW
155-206	cons.	97 LLSPRGSRPSWGPDPRTTSRNLCKVIDITCgFADLMGYIPLVGAPlGGVaRAlAEGTVyLEDGvVATGM1PGCSFSIFILLSClTvPasa
155-176	type 1	LLSPRGSRPSWGPDPRTTSRNLCKVIDITCgFADLMGYIPLVGAPlGGVaRAlAEGTVyLEDGvVATGM1PGCSFSIFILLSClTvPasa
177-186	type 2	LLSPRGSRPSWGPDPRTTSRNLCKVIDITCgFADLMGYIPLVGAPlGGVaRAlAEGTVyLEDGvVATGM1PGCSFSIFILLSClTvPasa
187-190	type 3	LLSPRGSRPSWGPDPRTTSRNLCKVIDITCgFADLMGYIPLVGAPlGGVaRAlAEGTVyLEDGvVATGM1PGCSFSIFILLSClTvPasa
191-197	type 4	LLSPRGSRPSWGPDPRTTSRNLCKVIDITCgFADLMGYIPLVGAPlGGVaRAlAEGTVyLEDGvVATGM1PGCSFSIFILLSClTvPasa
198-205	type 5	LLSPRGSRPSWGPDPRTTSRNLCKVIDITCgFADLMGYIPLVGAPlGGVaRAlAEGTVyLEDGvVATGM1PGCSFSIFILLSClTvPasa
206	type 6	LLSPRGSRPSWGPDPRTTSRNLCKVIDITCgFADLMGYIPLVGAPlGGVaRAlAEGTVyLEDGvVATGM1PGCSFSIFILLSClTvPasa